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     FILE 'HCAPLUS' ENTERED AT 13:42:39 ON 10 JUN 2010
L1          1369 S BRANCHING ENZYME
L2         44820 S MAIZE
L3           263 S L1 AND L2
L4            96 S L3 AND (PY<2000 OR AY<2000 OR PRY<2000)
L5           808 S (BRANCHING ENZYME)(4A)(STARCH)
L6           851 S (BRANCHING ENZYME)(4A)(STARCH OR AMYLOSE OR AMYLOPECTIN)
L7           231 S L2 AND L6
L8            71 S L7 AND (PY<2000 OR AY<2000 OR PRY<2000)
L9       2911043 S EXPRESSION OR EXPRESSED OR (DEGREE OF BRANCHING) OR (BRANCHIN
L10           60 S L8 AND L9
L11      1540936 S EXPRESSION OR EXPRESSED OR (DEGREE OF BRANCHING) OR (BRANCHIN
L12           33 S L8 AND L11
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=> file hcaplus
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.22       0.22

FILE 'HCAPLUS' ENTERED AT 10:47:58 ON 10 JUN 2010
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FILE COVERS 1907 - 10 Jun 2010  VOL 152 ISS 24
FILE LAST UPDATED: 9 Jun 2010  (20100609/ED)
REVISED CLASS FIELDS (/NCL) LAST RELOADED:  Apr 2010
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE:  Apr 2010

HCAplus now includes complete International Patent Classification (IPC)
reclassification data for the second quarter of 2010.

CAS Information Use Policies apply and are available at:

http://www.cas.org/legal/infopolicy.html

This file contains CAS Registry Numbers for easy and accurate
substance identification.

=> s branching enzyme
        65463 BRANCHING
       937081 ENZYME
L1       1369 BRANCHING ENZYME
                (BRANCHING(W)ENZYME)

=> s algae or algal or reinhardtt or reinhardti
        55914 ALGAE
        24232 ALGAL
            1 REINHARDTT
         2734 REINHARDTI
L2      69842 ALGAE OR ALGAL OR REINHARDTT OR REINHARDTI

=> s l1 and l2
L3         22 L1 AND L2

=> d l3 1-22 ti abs bib

L3   ANSWER 1 OF 22  HCAPLUS  COPYRIGHT 2010 ACS on STN
TI   Starch biosynthesis in plants
AB   A review.  Starch is a major storage compound in plants that is present both
     in leaves and in storage tissues.  Biochem. and mol. biol. data show that
     ADP-glucose is the glucosyl donor for plant starch synthesis, and its
     synthesis is catalyzed by ADP-glucose pyrophosphorylase.  Subsequently,
     starch synthases catalyze the transfer of the glucosyl residue from
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ADP-glucose to the oligosaccharide chains of the starch components amylose and amylopectin to form new α-1,4-glucosidic residues. After elongation of these α-1,4-glucosidic chains, the branching enzyme catalyzes a cleavage of the elongated chain and transfers the cleaved portion of the oligosaccharide chain to either another region in the amylopectin mol. or to a new amylopectin and forms a new α-1,6-glucosidic linkage. Amylose synthesis is catalyzed by the granule-bound starch synthase. Regulation of starch synthesis occurs at the ADP-glucose pyrophosphorylase step. The enzyme from higher plants, green algae, and cyanobacteria is activated allosterically by 3-phosphoglycerate and inhibited by inorg. phosphate. Isolation of mutants and control analyses indicate that the allosteric activation and inhibition are of physiol. and functional importance in the regulation of starch synthesis. Furthermore, evidence indicates that ADP-glucose pyrophosphorylases can also be regulated by a redox mechanism. The current knowledge of the enzyme structures and critical amino acids necessary for substrate binding, allosteric effector binding, regulation, and catalysis for the ADP-glucose pyrophosphorylase is reviewed.

AN 2009:1026885 HCAPLUS <<LOGINID::20100610>>
DN 152:376834
TI Starch biosynthesis in plants
AU Preiss, Jack
CS Department of Biochemistry and Molecular Biology, Michigan State University, East Lansing, MI, USA
SO Wiley Encyclopedia of Chemical Biology (2009), Volume 4, 362-376. Editor(s): Begley, Tadhg P. Publisher: John Wiley & Sons, Inc., Hoboken, N. J.
CODEN: 69LUOU; ISBN: 978-0-471-75477-0
DT Conference; General Review
LA English
RE.CNT 144 THERE ARE 144 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 2 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Chlorella starch branching enzyme II (BEII) can complement the function of BEIIb in rice endosperm
AB In monocots, starch branching enzyme II (BEII) was functionally differentiated into BEIIa and BEIIb after separation from the dicots, and in cereals BEIIb plays a distinct role in amylopectin biosynthesis in the endosperm. The present study was conducted to examine to what extent a green algal BEII has an overlapping function with BEIIb in starch biosynthesis by introducing the Chlorella BEII gene into an amylose-extender (ae) mutant of rice. Chlorella BEII was found to complement the contribution of the rice endosperm BEIIb to the structures of amylopectin and starch granules because these mutated phenotypes were recovered almost completely to those of the wild type by the expression of Chlorella BEII. When the recombinant BE enzymes were incubated with the rice ae amylopectin, the branching pattern of Chlorella BEII was much more similar to that of rice BEIIb rather than rice BEIIa. Detailed analyses of BE reaction products suggests that BEIIb and Chlorella BEII only transfer chains with a d.p. (DP) of 6 and 7, whereas BEIIa preferably transfers short chains with a DP of about 6-11. These results show that the Chlorella BEII is functionally similar to rice BEIIb rather than BEIIa.
AN 2009:735243 HCAPLUS <<LOGINID::20100610>>
DN 151:354291
TI Chlorella starch branching enzyme II (BEII) can complement the function of BEIIb in rice endosperm
AU Sawada, Takayuki; Francisco, Perigio B., Jr.; Aihara, Satomi; Utsumi, Yoshinori; Yoshida, Mayumi; Oyama, Yasunori; Tsuzuki, Mikio; Satoh, Hikaru; Nakamura, Yasunori

CS CREST, Japan Science and Technology Corporation, Kawaguchi, Saitama, 332-0012, Japan
SO Plant and Cell Physiology (2009), 50(6), 1062-1074
CODEN: PCPHA5; ISSN: 0032-0781
PB Oxford University Press
DT Journal
LA English
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 3 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Manufacture of branched carbohydrate using branching enzyme and application in food
AB Branched α-glucan of (d.p., 5-15) is manufactured from α-glucan-containing starch hydrolyzate with branching enzyme such as α-amylase. The branching enzyme is obtained from rice, corn, potato, algae, etc. The branched α-glucan is useful for making food such as syrup.
AN 2009:701978 HCAPLUS <<LOGINID::20100610>>
DN 150:562162
TI Manufacture of branched carbohydrate using branching enzyme and application in food
IN Ohata, Yuichiro; Yamamoto, Takeshi; Nakamura, Yasunori; Fujita, Naoko; Nakakuki, Teruo
PA Akita Prefectural University, Japan; Nihon Shokuhin Kako Co., Ltd.
SO Jpn. Kokai Tokkyo Koho, 15pp.
CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI JP 2009124994	A	20090611	JP 2007-303256	20071122
PRAI JP 2007-303256		20071122		

L3 ANSWER 4 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI The phenotype of soluble starch synthase IV defective mutants of Arabidopsis thaliana suggests a novel function of elongation enzymes in the control of starch granule formation
AB All plants and green algae synthesize starch through the action of the same five classes of elongation enzymes: the starch synthases. Arabidopsis mutants defective for the synthesis of the soluble starch synthase IV (SSIV) type of elongation enzyme have now been characterized. The mutant plants displayed a severe growth defect but nonetheless accumulated near to normal levels of polysaccharide storage. Detailed structural anal. has failed to yield any change in starch granule structure. However, the number of granules per plastid has dramatically decreased leading to a large increase in their size. These results, which distinguish the SSIV mutants from all other mutants reported to date, suggest a specific function of this enzyme class in the control of granule nos. We speculate therefore that SSIV could be selectively involved in the priming of starch granule formation.
AN 2007:248135 HCAPLUS <<LOGINID::20100610>>
DN 147:5811
TI The phenotype of soluble starch synthase IV defective mutants of Arabidopsis thaliana suggests a novel function of elongation enzymes in the control of starch granule formation
AU Roldan, Isaac; Wattebled, Fabrice; Lucas, M. Mercedes; Delvalle, David; Planchot, Veronique; Jimenez, Sebastian; Perez, Ricardo; Ball, Steven; D'Hulst, Christophe; Merida, Angel
CS Instituto de Bioquimica Vegetal y Fotosintesis, CSIC-US, Seville, 41092,

Spain
SO Plant Journal (2007), 49(3), 492-504
CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Publishing Ltd.
DT Journal
LA English
OSC.G 21 THERE ARE 21 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 5 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Common evolutionary origin of starch biosynthetic enzymes in green and red algae
AB Plastidic starch synthesis in green algae and plants occurs via ADP-glucose in likeness to prokaryotes from which plastids have evolved. In contrast, floridean starch synthesis in red algae proceeds via uridine diphosphate-glucose in semblance to eukaryotic glycogen synthesis and occurs in the cytosol rather than the plastid. Given the monophyletic origin of all plastids, we investigated the origin of the enzymes of the plastid and cytosolic starch synthetic pathways to determine whether their location reflects their origin-either from the cyanobacterial endosymbiont or from the eukaryotic host. We report that, despite the compartmentalization of starch synthesis differing in green and red lineages, all but one of the enzymes of the synthetic pathways shares a common origin. Overall, the pathway of starch synthesis in both lineages represents a chimera of the host and endosymbiont glycogen synthesis pathways. Moreover, host-derived proteins function in the plastid in green algae, whereas endosymbiont-derived proteins function in the cytosol in red algae. This complexity demonstrates the impacts of integrating pathways of host with those of both primary and secondary endosymbionts during plastid evolution.
AN 2006:69305 HCAPLUS <<LOGINID::20100610>>
DN 145:392317
TI Common evolutionary origin of starch biosynthetic enzymes in green and red algae
AU Patron, Nicola J.; Keeling, Patrick J.
CS Canadian Institute for Advanced Research, Botany Department, University of British Columbia, Vancouver, BC, V6T 1Z4, Can.
SO Journal of Phycology (2005), 41(6), 1131-1141
CODEN: JPYLAJ; ISSN: 0022-3646
PB Blackwell Publishing, Inc.
DT Journal
LA English
OSC.G 21 THERE ARE 21 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)
RE.CNT 75 THERE ARE 75 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 6 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Polyglucan synthase gene knockout Cyanobacterium and use in screening the effects of heterologous genes on α-polyglucan biosynthesis
AB Polyglucan synthase gene knockout blue-green algae and use in screening the effects of heterologous genes on α-polyglucan biosynthesis, is disclosed. Cyanobacterium Synechococcus sp. PCC7942 deficient in the gene coding for glycogen synthase (GS), glycogen branching enzyme (BE), or isoamylase (ISA), were generated.
AN 2004:819634 HCAPLUS <<LOGINID::20100610>>
DN 141:308640
TI Polyglucan synthase gene knockout Cyanobacterium and use in screening the effects of heterologous genes on α-polyglucan biosynthesis
IN Suzuki, Eiji; Moriya, Katsuya; Takahashi, Junichiro; Kudo, Haruka;

Nakamura, Yasunori
PA Japan Science and Technology Agency, Japan
SO Jpn. Kokai Tokkyo Koho, 99 pp.
CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI JP 2004275050	A	20041007	JP 2003-69795	20030314
JP 4267942	B2	20090527		
PRAI JP 2003-69795		20030314		

L3 ANSWER 7 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI A transformed plant having a reduced endogenous starch branching enzyme activity and a heterologous glucan branching enzyme and its use for production of starch
AB The present invention relates to a transformed plant having a reduced endogenous starch branching enzyme (SBE) activity, and having a heterologous glucan branching enzyme (GBE) activity. The invention also relates to starch obtainable from such a plant. Reduction of potato SBE activity by antisense SBE I and SBE II expression is described. Cloning and sequencing of SBE from the red alga Gracilaria lemaneiformis and heterologous expression of the enzyme in potato tubers are reported. Gene, and encoded amino acid sequences of the G. lemaneiformis SBE are disclosed. Heterologous expression of a glycogen branching enzyme from E. coli in potato tubers is described. Production of floridean-starch types and glycogen-starch types in transgenic potatoes using the heterologously expressed G. lemaneiformis SBE and glycogen branching enzyme from E. coli resp. is described.
AN 2001:713525 HCAPLUS <<LOGINID::20100610>>
DN 135:268185
TI A transformed plant having a reduced endogenous starch branching enzyme activity and a heterologous glucan branching enzyme and its use for production of starch
IN Poulson, Peter; Sorensen, Iben Schildt
PA Danisco A/s, Den.
SO PCT Int. Appl., 51 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2001070942	A2	20010927	WO 2001-IB493	20010316
WO 2001070942	A3	20020404		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
GB 2360521	A	20010926	GB 2000-6733	20000320
CA 2402463	A1	20010927	CA 2001-2402463	20010316
EP 1265477	A2	20021218	EP 2001-914128	20010316
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				

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     US 20040068766       A1    20040408    US 2003-239145         20030115
PRAI GB 2000-6733         A     20000320
     WO 2001-IB493        W     20010316
OSC.G   3     THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT  4     THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3   ANSWER 8 OF 22  HCAPLUS  COPYRIGHT 2010 ACS on STN
TI   Fusion proteins with Chlamydomonas starch synthase and food and
     pharmaceuticals containing starch-fusion protein complexes
AB   The invention concerns starch granules containing a hybrid protein between a
     starch synthase and a protein of interest, the nucleotide sequences used
     for obtaining same, methods for preparing them and their uses, particularly
     in pharmaceutical compns.  Thus, the cDNA for the STA2 gene starch
     synthase of C. reinhardtii was cloned and sequenced.  A
     C-terminal-truncated starch synthase of 58 kilodaltons (wild-type enzyme:
     76 kilodaltons) encoded by the sta2-1 allele was found to have a six-fold
     increased Km for ADP-glucose and to bind to starch grains with unaltered
     affinity.
AN   2000:842295  HCAPLUS <<LOGINID::20100610>>
DN   134:14733
TI   Fusion proteins with Chlamydomonas starch synthase and food and
     pharmaceuticals containing starch-fusion protein complexes
IN   D'Hulst, Christophe; Ball, Steven
PA   Centre National de la Recherche Scientifique, Fr.
SO   PCT Int. Appl., 90 pp.
     CODEN: PIXXD2
DT   Patent
LA   French
FAN.CNT 1
     PATENT NO.            KIND   DATE        APPLICATION NO.        DATE
     --------------        ----   --------    -------------------    --------
PI   WO 2000071734         A1     20001130    WO 2000-FR1384         20000519
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR,
             CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU,
             ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU,
             LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD,
             SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU,
             ZA, ZW
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
             DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ,
             CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     FR 2793806             A1     20001124    FR 1999-6494           19990521
     FR 2793806             B1     20030425
     CA 2374416             A1     20001130    CA 2000-2374416        20000519
     EP 1179078             A1     20020213    EP 2000-929649         20000519
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO
     JP 2003500060          T      20030107    JP 2000-620111         20000519
     US 6982083             B1     20060103    US 2002-980771         20020110
PRAI FR 1999-6494           A      19990521
     WO 2000-FR1384         W      20000519
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G   2     THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT  9     THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3   ANSWER 9 OF 22  HCAPLUS  COPYRIGHT 2010 ACS on STN
TI   Modified starch metabolism enzymes and encoding genes for improvement and
     optimization of plant phenotypes
AB   The invention provides methods for generating, identifying, and selecting
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polynucleotides encoding novel starch metabolizing enzymes (NSME), NSME-encoding polynucleotides, compns. of recombinant shuffled NSME protein, plant cells and microbes containing a shuffled NSME polynucleotide in expressible form, plants containing a shuffled NSME polynucleotide in expressible form, novel starch compns. produced by said plants and cells, uses of such plants, cells, and starch compns. Thus, to create an ADP-glucose pyrophosphorylase with altered properties, the genes from E. coli and other microorganisms which have at least 70% sequence identity are randomly fragmented with DNase I and fragments of 100-300 bp are selected. These fragments are reassembled based on sequence similarity by primerless PCR. Recombination as well as variable levels of mutations that are introduced by the PCR reaction to generate the diversity. The assembled genes are cloned into a starch minus E. coli mutant that lacks the NSME. Transformed colonies expressing a functional NSME are screened for production of glycogen by iodine staining. Those colonies staining dark blue are presumed to contain deregulated NSME. Colonies expressing shuffled NSME genes are selected and grown in larger amts. in liquid culture and assayed for specific properties. Genes from those clones expressing one or more of the desired properties are iteratively shuffled in order to achieve optimization of one or more of the desired properties. The optimized gene is used to transform the desired crop plant in order to deregulate and increase starch biosynthesis in various tissues including tubers and seeds.

AN 2000:742226 HCAPLUS <<LOGINID::20100610>>
DN 133:291931
TI Modified starch metabolism enzymes and encoding genes for improvement and optimization of plant phenotypes
IN Stemmer, Willem P. C.; Subramanian, Venkitswaran; Raillard, Sun Ai; Huisman, Gjalt
PA Maxygen, Inc., USA
SO PCT Int. Appl., 71 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000061731	A2	20001019	WO 2000-US9840	20000412
WO 2000061731	A3	20010222		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 6703240	B1	20040309	US 2000-547844	20000412
PRAI US 1999-129009P	P	19990413		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 10 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Chimeric glycogen synthase gene-expressing transgenic plants with reduced starch loss at elevated growth temperature
AB Starch yield of wheat and maize plants grown under higher temps. than control plants is increased by the introduction of a chimeric gene comprising a glycogen synthase coding sequence under the control of a promoter directing expression and a terminator. A transit peptide for

translocation of the glycogen synthase to the plant plastid may also be included in the chimeric gene. The starch may also have altered processing characteristics, in particular an increased chain length. Thus, transgenic wheat and maize expressing a chimeric Escherichia coli glgA gene were produced. The chimeric gene consisted of the endosperm-specific high-mol.-weight glutenin gene promoter of wheat fused to the pea Rubisco small subunit transit peptide sequence fused to the glgA gene. Starch produced by these transgenic plants had an increased chain length. Addnl., seeds from these plants loss 8-11% less seed weight at 27° than did control plants.

AN 2000:666884 HCAPLUS <<LOGINID::20100610>>
DN 133:249926
TI Chimeric glycogen synthase gene-expressing transgenic plants with reduced starch loss at elevated growth temperature
IN Burrell, Michael Meyrick; Hedley, Clare
PA Advanced Technologies (Cambridge) Limited, UK
SO PCT Int. Appl., 76 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000055331	A1	20000921	WO 2000-GB848	20000309
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2365279	A1	20000921	CA 2000-2365279	20000309
EP 1165802	A1	20020102	EP 2000-907849	20000309
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
PRAI GB 1999-5698	A	19990312		
WO 2000-GB848	W	20000309		

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 11 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Biosynthesis of altered starch in genetically modified plants with glycogen branching enzyme gene
AB A method and compns. for altering starch properties in wheat and maize plants, starch obtained by such method, and transgenic plants producing such starch, are disclosed. Starch with altered properties is produced by introducing a gene construct comprising a glycogen branching enzyme coding sequence under the control of a promoter directing expression and a terminator. A transit peptide for translocation of the glycogen branching enzyme to the plant plastid may also be included in the chimeric gene construct. The starch has altered processing characteristics, in particular an decreased chain length. A chimeric gene containing the High Mol. Weight Glutenin (HMWG) promoter, nopaline synthase terminator, and the transit-peptide region of the small-subunit of the ribulose bisphosphate carboxylase (ssu of Rubisco) gene was utilized to direct expression of Escherichia coli glycogen branching enzyme (glgB) to wheat and maize. Expression of the glgB gene product in wheat and maize grain was detected by

immunoblot anal. Anal. of the starch from these transgenic wheat and maize lines indicated an decrease in chain length, particularly an increase in chain length between 5 and 8 glucose units. The above parameters indicate a novel wheat and maize starch based on expression of the glgB E. coli gene product in transgenic plants.

AN 2000:368616 HCAPLUS <<LOGINID::20100610>>
DN 133:29689
TI Biosynthesis of altered starch in genetically modified plants with glycogen branching enzyme gene
IN Burrell, Michael Meyrick
PA Advanced Technologies (Cambridge) Limited, UK
SO PCT Int. Appl., 56 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000031282	A1	20000602	WO 1999-GB3762	19991108
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				

PRAI GB 1998-25262 A 19981119
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 12 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Biosynthesis of altered starch in genetically modified plants with glycogen synthase gene
AB A method and compns. for altering starch properties in wheat and maize plants , starch obtained by such method, and transgenic plants producing such starch, are disclosed. Starch with altered properties is produced by introducing a gene construct comprising a glycogen synthase coding sequence under the control of a promoter directing expression and a terminator. A transit peptide for translocation of the glycogen synthase to the plant plastid may also be included in the chimeric gene construct. The starch has altered processing characteristics, in particular an increased chain length. A chimeric gene containing the High Mol. Weight Glutenin
(HMWG) promoter, nopaline synthase terminator, and the transit-peptide region of the small-subunit of the ribulose bisphosphate carboxylase (ssu of Rubisco) gene was utilized to direct expression of Escherichia coli glycogen synthase (glgA) to wheat and maize. Expression of the glgA gene product in wheat and maize grain was detected by immunoblot anal. Anal. of the starch from these transgenic wheat and maize lines indicated an increase in chain length, particularly in chain length between 17 and 28 glucose units. Rapid viscometric anal. yielded lower peak and final viscosity values (about 30% of control values), whereas differential scanning calorimetry values indicated increased enthalpy values. The above parameters indicate a novel wheat and maize starch based on expression of the glgA E. coli gene product in transgenic plants.
AN 2000:368603 HCAPLUS <<LOGINID::20100610>>
DN 133:29688
TI Biosynthesis of altered starch in genetically modified plants with glycogen synthase gene

IN Burrell, Michael Meyrick
PA Advanced Technologies (Cambridge) Limited, UK
SO PCT Int. Appl., 66 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000031274	A1	20000602	WO 1999-GB3734	19991109
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	CA 2349819	A1	20000602	CA 1999-2349819	19991109
	CA 2349819	C	20080909		
	EP 1131442	A1	20010912	EP 1999-954197	19991109
	EP 1131442	B1	20100526		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, CY				
	US 6468799	B1	20021022	US 1999-444728	19991118
	AU 2000010616	A	20000807	AU 2000-10616	20000119
	AU 2004202150	A1	20040617	AU 2004-202150	20040519
	AU 2004202150	B2	20060713		
PRAI	GB 1998-25242	A	19981119		
	WO 1999-GB3734	W	19991109		
	AU 2000-10616	A3	20000119		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 13 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Method for the preparation of a mixture of starch branching enzymes using a mutant of the green algae Chlamydomonas reinhardtii
AB The invention concerns a method for obtaining a mixture of starch branching enzymes extracted from unicellular algae characterized in that it consists in modifying a unicellular algae such that it no longer expresses a starch debranching activity; in treating said modified unicellular algae so as to obtain a concentrated acellular extract; and in subjecting said concentrated acellular extract to mol. sieving so as to obtain a mixture of starch branching enzymes extracted from algae. Thus the wild type green algae Chlamydomonas reinhardtii was mutated on the sta7 locus by inserting the pARG7 plasmid carrying the argininosuccinate lyase coding sequence. The obtained phenotype was lacking starch debranching enzyme activity. The mutant was used for fermentation in 10 L scale to produce starch branching enzymes I and II. After cell disruption in a French press, the extract was purified in several steps and used for amylopectin modification.
AN 2000:227757 HCAPLUS <<LOGINID::20100610>>
DN 132:235980
TI Method for the preparation of a mixture of starch branching enzymes using a mutant of the green algae Chlamydomonas reinhardtii
IN Fleche, Guy; Looten, Philippe; Heysen, Arnaud; Ball, Steven
PA Roquette Freres, Fr.
SO PCT Int. Appl., 29 pp.

CODEN: PIXXD2
DT Patent
LA French
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000018893	A1	20000406	WO 1999-FR2261	19990923
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
FR 2783838	A1	20000331	FR 1998-12051	19980925
FR 2783838	B1	20001201		
CA 2345331	A1	20000406	CA 1999-2345331	19990923
AU 9956320	A	20000417	AU 1999-56320	19990923
EP 1115843	A1	20010718	EP 1999-943032	19990923
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
PRAI FR 1998-12051	A	19980925		
WO 1999-FR2261	W	19990923		

OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 14 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Cloning and characterization of a nuclear gene encoding a starch-branching enzyme from the marine red alga Gracilaria gracilis
AB The biosynthesis of starch in red algae occurs in the cytosol, in contrast to green plants where it takes place in the plastid. We have cloned a nuclear gene from the red alga Gracilaria gracilis that encodes a homolog of starch-branching enzymes (SBEs); this gene, which is apparently intron-free, was designated as GgSBE1. A potential TATA box, CAAT boxes, and other potential regulatory elements were observed in its 5' flanking region. The encoded 766-aa peptide shares significant sequence similarity with SBEs from green plants (at least 40%), and with glycogen-branching enzymes (GBEs) from human (46%) and Saccharomyces cerevisiae (45%). Southern-hybridization anal. indicates that the gene is single-copy, although weaker signals suggest that related genes exist in the genome of G. gracilis. Phylogenetic analyses indicate that GgSBE1 groups within the eukaryote branching enzymes (BEs) and not with eubacterial GBEs, suggesting that its gene has not been derived directly from an endosymbiotic cyanobacterium, but instead is ancestrally eukaryotic.
AN 1998:549701 HCAPLUS <<LOGINID::20100610>>
DN 130:972
TI Cloning and characterization of a nuclear gene encoding a starch-branching enzyme from the marine red alga Gracilaria gracilis
AU Lluisma, A. O.; Ragan, M. A.
CS Institute for Marine Biosciences, National Research Council of Canada, Halifax, NS, B3H 3Z1, Can.
SO Current Genetics (1998), 34(2), 105-111
CODEN: CUGED5; ISSN: 0172-8083
PB Springer-Verlag
DT Journal
LA English
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)

RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 15 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI A Chlamydomonas reinhardtii low-starch mutant is defective for 3-phosphoglycerate activation and orthophosphate inhibition of ADP-glucose pyrophosphorylase
AB A low-starch mutant accumulating less than 5% of wild-type amts. was isolated after x-ray mutagenesis of C. reinhardtii cells. The recessive st-1-1 defect segregated as a single Mendelian mutation through meiosis, and led to a severe decrease in starch accumulation under all culture conditions tested, whether in the light or in darkness. Adenosine 5'-diphosphoglucose pyrophosphorylase (in the absence of 3-phosphoglycerate), starch synthase, phosphoglucomutase, phosphorylase, and starch-branching enzyme were all characterized and shown to be unaffected by the mutation. However, ADP-glucose pyrophosphorylase in the mutant had its sensitivity to activation by 3-phosphoglycerate lowered dramatically and became less responsive to orthophosphate. The results are consistent both with a mutation in a structural gene of a multisubunit enzyme or in a regulatory gene responsible for switching ADP-glucose pyrophosphorylase from a 3-phosphoglycerate-insensitive to a 3-phosphoglycerate-sensitive form. These results provide definite proof of the in vivo requirement for 3-phosphoglycerate activation to obtain substantial starch synthesis in plants. The conclusions hold both for synthesis from CO2 in the light or from exogenous organic C sources in darkness. A model is presented in which the existence of a 3-phosphoglycerate gradient explains localized starch synthesis around the pyrenoid of lower plants.
AN 1991:603057 HCAPLUS <<LOGINID::20100610>>
DN 115:203057
OREF 115:34553a,34556a
TI A Chlamydomonas reinhardtii low-starch mutant is defective for 3-phosphoglycerate activation and orthophosphate inhibition of ADP-glucose pyrophosphorylase
AU Ball, Steven; Marianne, Therese; Dirick, Leon; Fresnoy, Marc; Delrue, Brigitte; Decq, Andre
CS Lab. Chim. Biol., Univ. Sci. Tech. Lille Flandres-Artois, Villeneuve d'Ascq, F-59655, Fr.
SO Planta (1991), 185(1), 17-26
CODEN: PLANAB; ISSN: 0032-0935
DT Journal
LA English
OSC.G 51 THERE ARE 51 CAPLUS RECORDS THAT CITE THIS RECORD (51 CITINGS)

L3 ANSWER 16 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Polyglucan branching isoenzymes of algae
AB The isoenzyme nature of the branching enzymes involved in the formation of the storage polyglucans of 3 algal species was investigated by using the method of Hedrick and Smith (CA 69:41618a) to analyze the results of polyacrylamide gel electrophoresis mobility studies. The red alga, Rhodymenia pertusa, contains 2 enzymes which act only on amylose to form moderately branched amylopectin (Q enzymes), and 1 with dual activity acting on both amylose and amylopectin to form highly branched phytoglycogens. Both the cyanophyte, Oscillatoria princeps, and the unclassified alga, Cyanidium caldarium, contain 2 enzymes with dual activity of the latter type. Analyses of the mobilities indicated that all 7 are isoenzymes, differing only in elec. charge, and probably are related in an evolutionary sense. The results suggest that C. caldarium belongs with the cyanophytes, or is a transition form between the blueGreen and red algae.
AN 1971:84012 HCAPLUS <<LOGINID::20100610>>

DN 74:84012
OREF 74:13599a,13602a
TI Polyglucan branching isoenzymes of algae
AU Fredrick, Jerome F.
CS Res. Lab., Dodge Chem. Co., Bronx, NY, USA
SO Physiologia Plantarum (1971), 24(1), 55-8
CODEN: PHPLAI; ISSN: 0031-9317
DT Journal
LA English
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L3 ANSWER 17 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Evolution of polyglucoside-synthesizing isozymes in the algae
AB A review with 30 refs.
AN 1971:29083 HCAPLUS <<LOGINID::20100610>>
DN 74:29083
OREF 74:4683a,4688a
TI Evolution of polyglucoside-synthesizing isozymes in the algae
AU Fredrick, Jerome F.
CS Res. Lab., Dodge Chem. Co., Bronx, NY, USA
SO Annals of the New York Academy of Sciences (1970), 175(Article 2), 524-30
CODEN: ANYAA9; ISSN: 0077-8923
DT Journal; General Review
LA English

L3 ANSWER 18 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Biochemical evolution of glucosyl transferase isozymes in algae
AB Purified phosphorylase prepns. from Oscillatoria, Rhodymenia, and Spirogyra, upon polyacrylamide gel electrophoresis, had 5 protein densitometric peaks. The demarcations were less distinct in Rhodymenia. In Spirogyra, protein a4 diminished, while protein a2 appeared to combine with protein a3. Proteins a1 and a2 were phosphorylases, and were similar to the a and b phosphorylases of animal tissues. Traces of a1 appeared in Rhodymenia. Enzymes a3 and a4 were active on both uridine diphosphoglucose (I) and adenosine diphosphoglucose (II); they were present in purified phosphorylase prepns. of all 3 algae. The combined a3 and a2 enzyme in Spirogyra acted on I and II and glucose 1-phosphate. Fraction a4 diminished simultaneously. Protein a5 appeared to be a branching enzyme; it caused branching in amylose. Protein a5 was present in all 3 algae. ADP and UDP were released from nucleotide-glucose complexes.
AN 1968:493709 HCAPLUS <<LOGINID::20100610>>
DN 69:93709
OREF 69:17515a,17518a
TI Biochemical evolution of glucosyl transferase isozymes in algae
AU Fredrick, Jerome F.
CS Div. of New York Res. Lab., Dodge Chem. Co., Bronx, NY, USA
SO Annals of the New York Academy of Sciences (1968), 151(1), 413-23
CODEN: ANYAA9; ISSN: 0077-8923
DT Journal
LA English
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L3 ANSWER 19 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Multiple forms of polyglucoside-branching enzyme in the algae
AB Three isozymes specifically concerned with the branching of linear polyglucoside were detected in blue-green, red, and green algae, by using two-dimensional polyacrylamide-gel electrophoresis. Two isozymes were found in Oscillatoria princeps, three were present in Spirogyra setiformis, and two in red algae of the Rhodymenia species. The

degree of branching of the storage carbohydrate may be related to the evolutionary status of these algae.
AN 1968:102547 HCAPLUS <<LOGINID::20100610>>
DN 68:102547
OREF 68:19787a,19790a
TI Multiple forms of polyglucoside-branching enzyme in the algae
AU Fredrick, Jerome F.
CS Res. Lab., Dodge Chem. Co., Bronx, NY, USA
SO Physiologia Plantarum (1968), 21(1), 176-82
CODEN: PHPLAI; ISSN: 0031-9317
DT Journal
LA English

L3 ANSWER 20 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Effect of surface activity and chelation phenomena on the activity of the polyglucoside-synthesizing enzymes of Oscillatoria
AB A study was made of the effects of chelation and surface activity on the phosphorylase and the branching enzyme of the alga Oscillatoria princeps, as exhibited by the presence of both types of agents in the reaction mixts. (dipotassium salt of glucose-1-phosphate, 0.05M, NaHCO3 buffer, and primer mols. of 0.1% amylose), as well as of the influence of a cationic surfactant combining both chelation and surface activity within its mols. The materials and procedures used are described and the results obtained are tabulated, plotted, and discussed. The ionic surfactants greatly inhibited the phosphorylase and branching enzyme of Oscillatoria princeps. The cationic surfactant inhibited the phosphorylase to a larger extent than the branching enzyme. The polyglucosides synthesized by mixts. of phosphorylase and branching enzymes ranged from normal to mutant types depending on which enzyme was more inhibited. It was concluded that the activity of the branching enzyme was the deciding factor of the type of sugar synthesized by mixts. of the two enzymes. A mechanism was suggested whereby the ionic surfactants were first attracted to the active centers of the enzyme by the specific charges on the enzyme mols.; the micelle formation and physical blocking of these centers prevented the enzyme-substrate union. The chelation phenomena, with regard to enzyme activity, was found to be mainly a detoxifying action whereby the toxic metallic ions were disrupted from their union with the enzyme proteins and rendered inert by chelation, thus restoring full activity to the enzyme mols. 37 references.
AN 1958:113993 HCAPLUS <<LOGINID::20100610>>
DN 52:113993
OREF 52:20279h-i,20280a-c
TI Effect of surface activity and chelation phenomena on the activity of the polyglucoside-synthesizing enzymes of Oscillatoria
AU Fredrick, Jerome F.
CS Dodge Chem. Co., New York, NY
SO Physiologia Plantarum (1957), 10, 844-57
CODEN: PHPLAI; ISSN: 0031-9317
DT Journal
LA English

L3 ANSWER 21 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI The synthesis of polysaccharides in algae. V. Kinetics of polysaccharide formation in extracts of Oscillatoria princeps
AB cf. C.A. 47, 7609a. The application of reaction kinetics to the mixture of phosphorylase and branching enzyme in exts. from O. princeps must take into consideration the simultaneous action of both enzymes. The Ks of branching enzyme is about 20 times that of phosphorylase. The kinetic analysis of polyglucoside production

by the interaction of these 2 enzymes on glucose-1-phosphate becomes quite complex and gives only an approximation.
AN 1955:69693 HCAPLUS <<LOGINID::20100610>>
DN 49:69693
OREF 49:13377f-g
TI The synthesis of polysaccharides in algae. V. Kinetics of polysaccharide formation in extracts of Oscillatoria princeps
AU Frederick, Jerome F.
CS Treasury Dept. Lab., New York, NY
SO Physiologia Plantarum (1954), 7, 182-9
CODEN: PHPLAI; ISSN: 0031-9317
DT Journal
LA Unavailable

L3 ANSWER 22 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Synthesis of polysaccharides in the algae. III. Induction of polysaccharide variants in Oscillatoria princeps by low temperatures
AB The usual polysaccharide synthesized by O. princeps is highly branched like glycogen, but the culture of single strands at 5-10° gives rise to variants which have a different cytological structure and synthesize only an unbranched polysaccharide. Enzyme prepns. from these variants convert hexose phosphate to a straight-chain polysaccharide similar to amylose. Upon returning to 25-32° the low-temperature variants revert to a normal pattern of polysaccharide formation, but this treatment is without effect on the low-temperature enzyme exts. It is suggested that a gene controlling the synthesis of a branching enzyme is altered at 5° and reverts to normal at 25°.
AN 1953:45044 HCAPLUS <<LOGINID::20100610>>
DN 47:45044
OREF 47:7608i,7609a-b
TI Synthesis of polysaccharides in the algae. III. Induction of polysaccharide variants in Oscillatoria princeps by low temperatures
AU Frederick, Jerome F.
CS New York Univ., New York, NY
SO Physiologia Plantarum (1953), 6, 96-9
CODEN: PHPLAI; ISSN: 0031-9317
DT Journal
LA Unavailable

=> file hcaplus

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.22	0.22

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FILE COVERS 1907 - 10 Jun 2010 VOL 152 ISS 24
FILE LAST UPDATED: 9 Jun 2010 (20100609/ED)
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Apr 2010
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Apr 2010

HCAplus now includes complete International Patent Classification (IPC)
reclassification data for the second quarter of 2010.

This file contains CAS Registry Numbers for easy and accurate
substance identification.

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=> s branching enzyme
         65463 BRANCHING
        937081 ENZYME
L1        1369 BRANCHING ENZYME
                 (BRANCHING(W)ENZYME)

=> s maize
L2       44820 MAIZE

=> s l1 and l2
L3         263 L1 AND L2

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      20131408 PY<2000
       3717474 AY<2000
       3181945 PRY<2000
L4           96 L3 AND (PY<2000 OR AY<2000 OR PRY<2000)

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MISSING OPERATOR ENZYME) 4A
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s (branching enzyme)(4a starch
MISSING OPERATOR ENZYME)(4A
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

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        937081 ENZYME
          1369 BRANCHING ENZYME
                 (BRANCHING(W)ENZYME)
        202835 STARCH
L5         808 (BRANCHING ENZYME)(4A)(STARCH)

=> s (branching enzyme)(4a)(starch or amylose or amylopectin)
         65463 BRANCHING
        937081 ENZYME
          1369 BRANCHING ENZYME
                 (BRANCHING(W)ENZYME)
        202835 STARCH
         14914 AMYLOSE
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          8082 AMYLOPECTIN
L6         851 (BRANCHING ENZYME)(4A)(STARCH OR AMYLOSE OR AMYLOPECTIN)

=> s l2 and l6
L7         231 L2 AND L6

=> s l7 and (PY<2000 or AY<2000 or PRY<2000)
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L8           71 L7 AND (PY<2000 OR AY<2000 OR PRY<2000)

=> d l8 1-71 ti abs bib

L8   ANSWER 1 OF 71  HCAPLUS  COPYRIGHT 2010 ACS on STN
TI   Protein and cDNA sequences of corn gene dull1 coding for a starch synthase
     and use
AB   The maize gene dull1 (du1) of the present invention is a
     determinant of the structure of endosperm starch.  Mutations of du1 affect
     the activity of at least two enzymes involved in starch biosynthesis,
     namely the starch synthase, SSII, and the starch
     branching enzyme, SBEIIa.  Du1 codes for a predicted
     1674 residue protein, and is expressed with a unique temporal pattern in
     endosperm but is undetectable in leaf or root.  The size of the Du1
     product and its expression pattern match precisely the known
     characteristics of maize SSII.  The Du1 product contains two
     different repeated regions in its unique amino terminus, one of which is
     identical to a conserved segment of the starch debranching enzymes.  The
     cDNA provided for in the present invention encodes SSII, and mutations
     within this gene affect multiple aspects of starch biogenesis by
     disrupting an enzyme complex containing starch synthase(s),
     starch branching enzyme(s), and possibly
     starch debranching enzyme.
AN   2003:851297  HCAPLUS <<LOGINID::20100610>>
DN   139:334824
TI   Protein and cDNA sequences of corn gene dull1 coding for a starch synthase
     and use
IN   Myers, Alan M.; James, Martha Graham
PA   Iowa State University Research Foundation, Inc., USA
SO   U.S., 56 pp., Cont.-in-part of U.S. Ser. No. 968,542.
     CODEN: USXXAM
DT   Patent
LA   English
FAN.CNT 2
     PATENT NO.          KIND   DATE        APPLICATION NO.        DATE
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PI   US 6639125           B1    20031028    US 2000-554467         20000512 <--
     US 5981728           A     19991109    US 1997-968542         19971112 <--
     WO 9924575           A1    19990520    WO 1998-US24225        19981112 <--
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             SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN
         RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,
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PRAI US 1997-968542       A2    19971112  <--
     WO 1998-US24225      W     19981112  <--
     US 2000-554467       A1    20000512
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
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OSC.G   1     THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT  16    THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8   ANSWER 2 OF 71  HCAPLUS  COPYRIGHT 2010 ACS on STN
TI   The rice actin 2 promoter and intron and their use for plant
     transformation
AB   The current invention provides regulatory regions from the rice actin 2
     gene.  In particular, the current invention provides the rice actin 2
     promoter and actin 2 intron.  Compns. comprising these sequences are
     described, as well as transformation constructs derived therefrom.
     Further provided are methods for the expression of transgenes in plants
     comprising the use of these sequences.  The methods of the invention
     include the direct creation of transgenic plants with the rice actin 2
     intron and/or promoter directly by genetic transformation, as well as by
     plant breeding methods.  The actin 2 sequences of the invention represent
     a valuable new tool for the creation of transgenic plants, preferably
     having one or more added beneficial characteristics.
AN   2000:824429  HCAPLUS <<LOGINID::20100610>>
DN   133:359795
TI   The rice actin 2 promoter and intron and their use for plant
     transformation
IN   McElroy, David; Wu, Ray
PA   Dekalb Genetics Corporation, USA; Cornell Research Foundation, Inc.
SO   PCT Int. Appl., 180 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
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PI   WO 2000070067       A1     20001123    WO 2000-US13303         20000512 <--
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             ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU,
             LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE,
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             CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     US 6429357           B1     20020806    US 1999-312304          19990514 <--
     CA 2372859           A1     20001123    CA 2000-2372859         20000512 <--
     EP 1179081           A1     20020213    EP 2000-942636          20000512 <--
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO
     EP 2123764           A1     20091125    EP 2009-169512          20000512 <--
         R:  AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC,
             NL, PT, SE
PRAI US 1999-312304       A1     19990514  <--
     EP 2000-942636       A3     20000512
     WO 2000-US13303      W      20000512
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G   3     THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT  8     THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8   ANSWER 3 OF 71  HCAPLUS  COPYRIGHT 2010 ACS on STN
TI   Branched glucose soluble polymers and method for the production thereof
AB   The invention relates to glucose soluble polymers which do not substantially
     contain any β-glucosidic bonds, characterized in that they comprise
     2.5-10% α-1,6 glucosidic bonds, have a very low or zero tendency to
```

retrograde in an aqueous solution determined according to a test A, possess an
MP
which is determined according to a test C having a median value of the distribution profile of the mol. masses ranging from 104 and 105 Daltons and have a reducing sugar content that is at most 9%. The polymers could prepared from waxy maize starch by heating and degrading with enzyme.

AN 2000:790550 HCAPLUS <<LOGINID::20100610>>
DN 133:351718
TI Branched glucose soluble polymers and method for the production thereof
IN Caboche, Jean-jacques; Looten, Philippe; Petitjean, Carole; Fleche, Guy; Comini, Serge; Backer, Daniel
PA Roquette Freres, Fr.
SO PCT Int. Appl., 33 pp.
CODEN: PIXXD2
DT Patent
LA French
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 2000066633	A1	20001109	WO 2000-FR1109	20000426	<--
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW					
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG					
	FR 2792941	A1	20001103	FR 1999-5523	19990430	<--
	FR 2792941	B1	20010727			
	CA 2371185	A1	20001109	CA 2000-2371185	20000426	<--
	EP 1177216	A1	20020206	EP 2000-922758	20000426	<--
	EP 1177216	B1	20040825			
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO					
	JP 2002543248	T	20021217	JP 2000-615661	20000426	<--
	AT 274525	T	20040915	AT 2000-922758	20000426	<--
	AU 777378	B2	20041014	AU 2000-43052	20000426	<--
	PT 1177216	E	20050131	PT 2000-922758	20000426	<--
	ES 2226821	T3	20050401	ES 2000-922758	20000426	<--
	CN 1197878	C	20050420	CN 2000-806938	20000426	<--
	NO 2001005224	A	20011025	NO 2001-5224	20011025	<--
	MX 2001011078	A	20020722	MX 2001-11078	20011030	<--
	KR 803833	B1	20080214	KR 2001-713894	20011030	<--
PRAI	FR 1999-5523	A	19990430	<--		
	WO 2000-FR1109	W	20000426			

OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 4 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Biosynthesis of altered starch in genetically modified plants with glycogen branching enzyme gene
AB A method and compns. for altering starch properties in wheat and maize plants, starch obtained by such method, and transgenic plants producing such starch, are disclosed. Starch with altered properties is produced by introducing a gene construct comprising a glycogen branching enzyme coding sequence under the control of a promoter directing expression and a terminator. A transit peptide for translocation of the glycogen branching enzyme to the plant plastid may

also be included in the chimeric gene construct. The starch has altered processing characteristics, in particular an decreased chain length. A chimeric gene containing the High Mol. Weight Glutenin (HMWG) promoter, nopaline synthase terminator, and the transit-peptide region of the small-subunit of the ribulose bisphosphate carboxylase (ssu of Rubisco) gene was utilized to direct expression of Escherichia coli glycogen branching enzyme (glgB) to wheat and maize. Expression of the glgB gene product in wheat and maize grain was detected by immunoblot anal. Anal. of the starch from these transgenic wheat and maize lines indicated an decrease in chain length, particularly an increase in chain length between 5 and 8 glucose units. The above parameters indicate a novel wheat and maize starch based on expression of the glgB E. coli gene product in transgenic plants.

AN 2000:368616 HCAPLUS <<LOGINID::20100610>>
DN 133:29689
TI Biosynthesis of altered starch in genetically modified plants with glycogen branching enzyme gene
IN Burrell, Michael Meyrick
PA Advanced Technologies (Cambridge) Limited, UK
SO PCT Int. Appl., 56 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000031282	A1	20000602	WO 1999-GB3762	19991108 <--
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				

PRAI GB 1998-25262 A 19981119 <--
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 5 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Biosynthesis of altered starch in genetically modified plants with glycogen synthase gene
AB A method and compns. for altering starch properties in wheat and maize plants , starch obtained by such method, and transgenic plants producing such starch, are disclosed. Starch with altered properties is produced by introducing a gene construct comprising a glycogen synthase coding sequence under the control of a promoter directing expression and a terminator. A transit peptide for translocation of the glycogen synthase to the plant plastid may also be included in the chimeric gene construct. The starch has altered processing characteristics, in particular an increased chain length. A chimeric gene containing the High Mol. Weight Glutenin (HMWG) promoter, nopaline synthase terminator, and the transit-peptide region of the small-subunit of the ribulose bisphosphate carboxylase (ssu of Rubisco) gene was utilized to direct expression of Escherichia coli glycogen synthase (glgA) to wheat and maize. Expression of the glgA gene product in wheat and maize grain was detected by immunoblot anal. Anal. of the starch from these transgenic wheat and maize lines indicated

an increase in chain length, particularly in chain length between 17 and 28 glucose units. Rapid viscometric anal. yielded lower peak and final viscosity values (about 30% of control values), whereas differential scanning calorimetry values indicated increased enthalpy values. The above parameters indicate a novel wheat and maize starch based on expression of the glgA E. coli gene product in transgenic plants.

AN 2000:368603 HCAPLUS <<LOGINID::20100610>>
DN 133:29688
TI Biosynthesis of altered starch in genetically modified plants with glycogen synthase gene
IN Burrell, Michael Meyrick
PA Advanced Technologies (Cambridge) Limited, UK
SO PCT Int. Appl., 66 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 2000031274	A1	20000602	WO 1999-GB3734	19991109	<--
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW					
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG					
	CA 2349819	A1	20000602	CA 1999-2349819	19991109	<--
	CA 2349819	C	20080909			
	EP 1131442	A1	20010912	EP 1999-954197	19991109	<--
	EP 1131442	B1	20100526			
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, CY					
	US 6468799	B1	20021022	US 1999-444728	19991118	<--
	AU 2000010616	A	20000807	AU 2000-10616	20000119	<--
	AU 2004202150	A1	20040617	AU 2004-202150	20040519	
	AU 2004202150	B2	20060713			
PRAI	GB 1998-25242	A	19981119	<--		
	WO 1999-GB3734	W	19991109	<--		
	AU 2000-10616	A3	20000119			

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 6 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Starch branching enzyme II (SBEII-1 and SBEII-2) isoforms from wheat, cDNA, transgenic plants, and altering starch properties for food use
AB A class of wheat SBEII genes, SBEII-1, recombinant protein expression in transgenic plants, and its use in altering properties of starch produced by a plant are claimed. Starch properties include the gelatinization onset and/or peak temperature The use of such starch with altered properties in food stuff, particularly bakery products is also claimed. CDNA clones for SBEII were isolated and sequenced. Those clones were divided into two sub-classes, SBEII-1 and SBEII-2 having sequence homol. to maize SBEIIb and SBEIIa, resp. These genes were mapped to the long arm of wheat group 2 homologous chromosomes. Some of those isoforms were expressed as recombinant protein in wheat. Differential scanning calorimetry studies

showed that starch produced in transgenic wheat transformed with expression construct for SBEII displayed higher onset, peak, and end temperature for gelatinization.

AN 2000:191230 HCAPLUS <<LOGINID::20100610>>

DN 132:247996

TI Starch branching enzyme II (SBEII-1 and SBEII-2) isoforms from wheat, cDNA, transgenic plants, and altering starch properties for food use

IN Goldsbrough, Andrew; Colliver, Steve

PA Plant Breeding International Cambridge Ltd., UK

SO PCT Int. Appl., 198 pp.
CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 2000015810	A1	20000323	WO 1999-GB3011	19990909	<--
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW					
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG					
	AU 9958725	A	20000403	AU 1999-58725	19990909	<--
	AU 767103	B2	20031030			
	EP 1117814	A1	20010725	EP 1999-946307	19990909	<--
	EP 1117814	B1	20100217			
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, CY					
	HU 2001003618	A2	20020128	HU 2001-3618	19990909	<--
	HU 2001003618	A3	20031229			
	AT 458061	T	20100315	AT 1999-946307	19990909	<--
	US 6730825	B1	20040504	US 2001-786480	20010917	<--
	US 20040216188	A1	20041028	US 2004-818770	20040406	<--
	US 7217857	B2	20070515			
	US 20080064864	A1	20080313	US 2007-788837	20070419	<--
	US 7465851	B2	20081216			
PRAI	EP 1998-307337	A	19980910	<--		
	WO 1999-GB3011	W	19990909	<--		
	US 2001-786480	A3	20010917			
	US 2004-818770	A3	20040406			

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 7 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Modern biotechnology and maize starch biosynthesis

AB A review with 23 refs. The application of transgenic plants, gene cloning of biotechnol. in maize industry has been studied. This review extensive summarizes the research on the maize starch biosynthetic pathway consisted of substrate (ADP-GLC) formation, chain elongation, branch point insertion and trimming and the role of ADP-glucose pyrophosphorylase (AGP), starch synthetase (SS), starch branching enzyme (SBE) and identified starch debranching enzyme (DBE). The perspective on maize structure, function and biosynthetic pathway has also been made.

AN 1999:803454 HCAPLUS <<LOGINID::20100610>>
DN 132:323209
TI Modern biotechnology and maize starch biosynthesis
AU Qin, Jian; Su, Dongmin; Wang, Hongyan; Wang, Jinshui
CS Food Engineering Department, Zhengzhou Grain College, Zhenghou, 450052, Peop. Rep. China
SO Zhengzhou Liangshi Xueyuan Xuebao (1999), 20(3), 81-85, 88
CODEN: ZLXUEN; ISSN: 1000-2332
PB Zhengzhou Liangshi Xueyuan Xuebao Bianjibu
DT Journal; General Review
LA Chinese

L8 ANSWER 8 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Expression control elements from the 5'- and 3'-regions of genes for starch branching enzymes
AB Regulatory elements from the 5'- and 3'-flanking regions of maize genes for starch branching enzymes (SbeI and Ae) are described for use in the expression of foreign genes in transgenic plants. The genes show different patterns of expression in tissues of the seed during its development and so the regulatory elements may be of use in the regulation of foreign gene expression in cereals. The genes were cloned by screening a genomic library with PCR products. The SbeI gene has a perfectly palindromic G-box in the promoter region while the Ae gene had elements resembling metal responsive elements, GC boxes, Hex, and I boxes. Functional anal. of the SbeI promoter identified sequences responsible for high level transcription and sugar regulation of gene expression. It also showed that elements within the transcribed region play a role in high level gene expression and that there sequences in the 5'-region that limit gene expression. An essential region of 60 bp was identified and shown to bind DNA-binding proteins.
AN 1999:795936 HCAPLUS <<LOGINID::20100610>>
DN 132:31802
TI Expression control elements from the 5'- and 3'-regions of genes for starch branching enzymes
IN Guiltinan, Mark J.; Kim, Kyung-Nam
PA The Pennsylvania State University, USA
SO PCT Int. Appl., 110 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9964562	A2	19991216	WO 1999-US13266	19990611 <--
	WO 9964562	A3	20000518		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	AU 9944384	A	19991230	AU 1999-44384	19990611 <--
PRAI	US 1998-89049P	P	19980612	<--	
	US 1998-89050P	P	19980612	<--	
	WO 1999-US13266	W	19990611	<--	

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 9 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Carbon isotope ratios of amylose, amylopectin and mutant starches
AB Carbon isotope ratios (expressed as δ13C values) were determined for various sources of starch and the starch fractions amylose and amylopectin. The δ13C values of amylose were consistently less neg., 0.4-2.3.permill., than those of amylopectin in kernel starch from maize (Zea mays) and barley (Hordeum vulgare) and in tuber starch from potato (Solanum tuberosum). Kernel starch isolated from the maize mutants wx1 and ae1, with known genetic lesions in the starch biosynthetic pathway, also showed significant differences in δ13C values. Collectively, these results suggest that variation in carbon isotope ratios in the amylose and amylopectin components of starch may be attributed to isotopic discrimination by the enzymes involved in starch biosynthesis.
AN 1999:737017 HCAPLUS <<LOGINID::20100610>>
DN 132:76065
TI Carbon isotope ratios of amylose, amylopectin and mutant starches
AU Scott, M. Paul; Jane, Jay-Lin; Soundararajan, Madhavan
CS USDA-ARS, Department of Agronomy, Iowa State University, Ames, IA, 50011, USA
SO Phytochemistry (1999), 52(4), 555-559
CODEN: PYTCAS; ISSN: 0031-9422
PB Elsevier Science Ltd.
DT Journal
LA English
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 10 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Expression of transgenes in plants using promoter and terminator sequences from Coix
AB Methods and compns. for the expression of transgenes in monocot plants including maize are disclosed. In the invention, gene silencing is avoided by use of monocot-homeologous sequences from plants of the genus Coix for transformation. Included in these transgene sequences are Coix promoters, enhancers, coding sequences and terminators. Suitable alternatives to maize-derived transgenes are desirable for expression in maize in that homol.-based gene silencing can limit or effectively eliminate transgene expression.
AN 1999:736897 HCAPLUS <<LOGINID::20100610>>
DN 131:347500
TI Expression of transgenes in plants using promoter and terminator sequences from Coix
IN Kriz, Alan L.; Luethy, Michael H.; Voyles, Dale A.
PA Dekalb Genetics Corporation, USA
SO PCT Int. Appl., 240 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9958659	A2	19991118	WO 1999-US10776	19990514 <--
	WO 9958659	A3	20000120		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,				

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            CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     US 6635806          B1    20031021    US 1998-78972          19980514 <--
     CA 2328129          A1    19991118    CA 1999-2328129        19990514 <--
     AU 9939957          A     19991129    AU 1999-39957          19990514 <--
     EP 1076706          A2    20010221    EP 1999-923112         19990514 <--
     EP 1076706          B1    20080206
          R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
              IE, FI, CY
     TR 2001000104       T2    20010621    TR 2001-104            19990514 <--
     BR 9910455          A     20011127    BR 1999-10455          19990514 <--
     JP 2002533057       T     20021008    JP 2000-548450         19990514 <--
     AT 385518           T     20080215    AT 1999-923112         19990514 <--
     PT 1076706          E     20080509    PT 1999-923112         19990514 <--
     ES 2301239          T3    20080616    ES 1999-923112         19990514 <--
     IN 2000DN00321      A     20080620    IN 2000-DN321          20001109 <--
     IN 227562           A1    20090130
     ZA 2000006576       A     20020213    ZA 2000-6576           20001113 <--
     MX 2000011199       A     20010419    MX 2000-11199          20001114 <--
     US 20050250938      A1    20051110    US 2003-660097         20030911 <--
     US 7256283          B2    20070814
     IN 2005DN05625      A     20070928    IN 2005-DN5625         20051205 <--
     US 20080271212      A1    20081030    US 2007-838724         20070814 <--
     US 20090013423      A1    20090108    US 2007-838725         20070814 <--
     US 20090199307      A1    20090806    US 2007-838721         20070814 <--
PRAI US 1998-78972       A1    19980514  <--
     WO 1999-US10776     W     19990514  <--
     IN 2000-DN321       A3    20001109
     US 2003-660097      A3    20030911
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G   5     THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)
RE.CNT  1     THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8   ANSWER 11 OF 71  HCAPLUS  COPYRIGHT 2010 ACS on STN
TI   Identification of cis-acting elements important for expression of the
     starch-branching enzyme I gene in
     maize endosperm
AB   The genes encoding the starch-branching enzymes (SBE) SBEI, SBEIIa, and
     SBEIIb in maize (Zea mays) are differentially regulated in
     tissue specificity and during kernel development.  To gain insight into
     the regulatory mechanisms controlling their expression, we analyzed the
     5'-flanking sequences of Sbe1 using a transient gene expression system.
     Although the 2.2-kb 5'-flanking sequence between -2,190 and +27 relative
     to the transcription initiation site was sufficient to promote
     transcription, the addition of the transcribed region between +28 and +228
     containing the first exon and intron resulted in high-level expression in
     suspension-cultured maize endosperm cells.  A series of 5'
     deletion and linker-substitution mutants identified two critical pos. cis
     elements, -314 to -295 and -284 to -255.  An electrophoretic
     mobility-shift assay showed that nuclear proteins prepared from
     maize kernels interact with the 60-bp fragment containing these two
     elements.  Expression of the Sbe1 gene is regulated by sugar concentration in
     suspension-cultured maize endosperm cells, and the region -314
     to -145 is essential for this effect.  Interestingly, the expression of
     mEmBP-1, a bZIP transcription activator, in suspension-cultured
     maize endosperm cells resulted in a 5-fold decrease in Sbe1
     promoter activity, suggesting a possible regulatory role of the G-box
     present in the Sbe1 promoter from -227 to -220.
AN   1999:615638  HCAPLUS <<LOGINID::20100610>>
DN   132:815
TI   Identification of cis-acting elements important for expression of the
```

starch-branching enzyme I gene in
maize endosperm
AU Kim, Kyung-Nam; Guiltinan, Mark J.
CS Intercollege Graduate Program in Plant Physiology, The Biotechnology Institute, and Department of Horticulture, The Pennsylvania State University, University Park, PA, 16802, USA
SO Plant Physiology (1999), 121(1), 225-236
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
OSC.G 17 THERE ARE 17 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)
RE.CNT 65 THERE ARE 65 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 12 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Maize starch synthase gene du1 and uses in starch production
AB Disclosed are the maize du1 gene, the encoded starch synthase isoenzyme II, and production of starch with recombinant du1-expressing cells or transgenic plants. The maize gene du11 (du1) of the present invention is a determinant of the structure of endosperm starch. Mutations of du1 affect the activity of at least two enzymes involved in starch biosynthesis, namely the starch synthase, SSII, and the starch branching enzyme, SBEIIa. Du1 codes for a predicted 1674 residue protein, and is expressed with a unique temporal pattern in endosperm but is undetectable in leaf or root. The size of the Du1 product and its expression pattern match precisely the known characteristics of maize SSII. The Du1 product contains two different repeated regions in its unique amino terminus, one of which is identical to a conserved segment of the starch debranching enzymes. The cDNA provided for in the present invention encodes SSII, and mutations within this gene affect multiple aspects of starch biogenesis by disrupting an enzyme complex containing starch synthase(s), starch branching enzyme(s), and possibly starch debranching enzyme(s).
AN 1999:326050 HCAPLUS <<LOGINID::20100610>>
DN 130:333760
TI Maize starch synthase gene du1 and uses in starch production
IN Myers, Alan M.; James, Martha G.
PA Iowa State University Research Foundation, Inc., USA
SO PCT Int. Appl., 138 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9924575	A1	19990520	WO 1998-US24225	19981112 <--
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 5981728	A	19991109	US 1997-968542	19971112 <--
CA 2309346	A1	19990520	CA 1998-2309346	19981112 <--
AU 9915236	A	19990531	AU 1999-15236	19981112 <--
AU 761419	B2	20030605		
EP 1030922	A1	20000830	EP 1998-959440	19981112 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,				

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            IE, FI
     BR 9814864          A     20011106    BR 1998-14864          19981112 <--
     JP 2001522604       T     20011120    JP 2000-520569         19981112 <--
     NZ 504534           A     20021220    NZ 1998-504534         19981112 <--
     MX 2000004586       A     20001110    MX 2000-4586           20000512 <--
     US 6639125          B1    20031028    US 2000-554467         20000512 <--
PRAI US 1997-968542      A     19971112  <--
     WO 1998-US24225     W     19981112  <--
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G   1     THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT  1     THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8   ANSWER 13 OF 71  HCAPLUS  COPYRIGHT 2010 ACS on STN
TI   Characterization of a gene encoding wheat endosperm starch
     branching enzyme-I
AB   A genomic DNA fragment from Triticum tauschii, the donor of the wheat D
     genome, contains a starch branching enzyme-I
     (SBE-I) gene spread over 6.5 kb.  This gene (designated wSBE I-D4) encodes
     an amino acid sequence identical to that determined for the N-terminus of SBE-I
     from the hexaploid wheat (T. aestivum) endosperm.  Cognate cDNA sequences
     for wSBE I-D4 were isolated from hexaploid wheat by hybridization
     screening from an endosperm library and also by PCR.  A contiguous
     sequence (D4 cDNA) was assembled from the sequence of five overlapping
     partial cDNAs which spanned wSBE I-D4.  D4 cDNA encodes a mature
     polypeptide of 87 kDa that shows 90% identity to SBE-I amino acid
     sequences from rice and maize and contains all the residues
     considered essential for activity.  D4 mRNA has been detected only in the
     endosperm and is at a maximum concentration mid-way through grain development.
 The
     wSBE I-D4 gene consists of 14 exons, similar to the structure for the
     equivalent gene in rice; the rice gene has a strikingly longer intron 2.  The
     3' end of wSBE I-D4 was used to show that the gene is located on group 7
     chromosomes.  The sequence upstream of wSBE I-D4 was analyzed with respect
     to conserved motifs.
AN   1999:177589  HCAPLUS <<LOGINID::20100610>>
DN   131:83671
TI   Characterization of a gene encoding wheat endosperm starch
     branching enzyme-I
AU   Rahman, S.; Li, Z.; Abrahams, S.; Abbott, D.; Appels, R.; Morell, M. K.
CS   CSIRO Plant Industry, Canberra, 2601, Australia
SO   Theoretical and Applied Genetics (1999), 98(1), 156-163
     CODEN: THAGA6; ISSN: 0040-5752
PB   Springer-Verlag
DT   Journal
LA   English
OSC.G   24    THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)
RE.CNT  32    THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8   ANSWER 14 OF 71  HCAPLUS  COPYRIGHT 2010 ACS on STN
TI   Molecular cloning and characterization of the Amylose-Extender
     gene encoding starch branching enzyme IIB in
     maize
AB   The amylose-extender (Ae) gene encoding starch-branching
     enzyme IIb (SBEIIb) in maize is predominantly expressed
     in endosperm and embryos during kernel development.  A maize
     genomic DNA fragment (-2964 to +20485) containing the Ae gene was isolated and
     sequenced.  The maize Ae mRNA is derived from 22 exons
     distributed over 16914 bp.  Twenty-one introns, differing in length from
     76 bp to 4020 bp, all have conserved junction sequences
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(GT··AG). Sequence anal. of the 5'- and 3'-flanking regions revealed a consensus TATA-box sequence located 28 bp upstream of the transcription initiation site as determined by primer extension anal., and a putative polyadenylation signal observed 29 bp upstream of the polyadenylation site based on cDNA sequence. Genomic Southern blot anal. suggests that a single Ae gene is present in the maize genome. Promoter activity was confirmed by testing a transcriptional fusion of the Ae 5'-flanking region between -2964 and +100 to a luciferase reporter gene in a transient expression assay using maize endosperm suspension cultured cells. 5' deletion anal. revealed that the 111 bp region from -160 to -50 is essential for high-level promoter activity.

AN 1999:44300 HCAPLUS <<LOGINID::20100610>>
DN 130:219005
TI Molecular cloning and characterization of the Amylose-Extender gene encoding starch branching enzyme IIB in maize
AU Kim, Kyung-Nam; Fisher, Dane K.; Gao, Ming; Guiltinan, Mark J.
CS Intercollege Graduate Programs in Plant Physiology and Genetics, The Biotechnology Institute, and Department of Horticulture, The Pennsylvania State University, University Park, PA, 16802, USA
SO Plant Molecular Biology (1998), 38(6), 945-956
CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer Academic Publishers
DT Journal
LA English
OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 15 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Arginine residue 384 at the catalytic center is important for branching enzyme II from maize endosperm
AB Starch-branching enzyme (BE) belongs to the amylolytic family which contains 4 highly conserved regions. These regions are proposed to play an important role in catalysis as they are thought to be necessary for catalysis and/or binding the substrate. Only 1 Arg residue was found to be conserved in a catalytic center at the same position in all known sequences of BEs from various species as well as in the α-amylase enzyme family. In maize BEII, a conserved Arg-384 residue is in catalytic region 2. Here, the authors used site-directed mutagenesis of Arg-384 in order to study its possible role in BE. Previous chemical modification studies suggested that it may play a role in substrate binding. Replacement of Arg-384 by Ala, Ser, Gln, and Glu in the active site caused almost total inactivation. However, a conservative mutation of the conserved Arg-384 residue by Lys resulted in some residual activity, .apprx.5% of that of the wild-type enzyme. The reaction kinetics of the purified mutant R384K enzyme were investigated and no large effect on the Km of the substrate, amylose, for BEII was observed Thus, these results suggest that conserved Arg-384 in maize BEII plays an important role in the catalytic function of BEs but may not be directly involved in substrate binding. (c) 1998 Academic Press.
AN 1998:797799 HCAPLUS <<LOGINID::20100610>>
DN 130:121370
TI Arginine residue 384 at the catalytic center is important for branching enzyme II from maize endosperm
AU Libessart, Nathalie; Preiss, Jack
CS Department of Biochemistry, Michigan State University, East Lansing, MI, 48824, USA
SO Archives of Biochemistry and Biophysics (1998), 360(1), 135-141
CODEN: ABBIA4; ISSN: 0003-9861
PB Academic Press

DT Journal
LA English
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 16 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Manipulating the starch composition of potato
AB A review with 41 refs. Starch can be fractionated into two types of glucose polymers: amylose and amylopectin. Amylose consists of essentially linear chains of α-(1,4)-linked glucose residues, whereas amylopectin is built up from α-(1,4)-linked chains with α-(1,6)-linked branches. The composition and fine structure of starch are responsible for many of the physicochem. properties and thus dets. its industrial uses. Variation in starch structure and composition can be found between and within crops. In the latter case it can be found in mutants, often resulting from the loss of function of one or more of the genes involved in starch biosynthesis. In maize, the most extensively studied crop, mutant genotypes are known for nearly every gene identified as being involved in starch biosynthesis. Differences in starch composition can also be achieved by genetic modifications such as antisense inhibition of genes or overexpression of (heterologous) genes. Most examples of genetic modification of starch composition are in potato, which can easily be transformed. Antisense inhibition of enzymes in the biosynthetic pathway, such as ADP glucose phosphorylase (AGP), (granule-bound) starch synthase or branching enzyme, lead to an altered starch content and/or composition In addition, the introduction and expression of bacterial genes, such as genes of the Escherichia coli glycogen synthesis pathway, in potato leads to starches with altered content, composition, structure and physicochem. properties. Studying the physicochem. properties of these altered starches will, together with the information obtained by research on starches of mutants, help to clarify the precise relationship between structural and functional features of starch.
AN 1998:787972 HCAPLUS <<LOGINID::20100610>>
DN 130:165463
TI Manipulating the starch composition of potato
AU Kortstee, A. J.; Flipse, E.; Kuipers, A. G. J.; Jacobsen, E.; Visser, R. G. F.
CS Graduate School of Experimental Plant Sciences, Department of Plant Breeding, Agricultural University Wageningen, Wageningen, 6700 AJ, Neth.
SO Portland Press Proceedings (1998), 14(Engineeering Crop Plants for Industrial End Uses), 89-98
CODEN: POPPEF; ISSN: 0966-4068
PB Portland Press Ltd.
DT Journal; General Review
LA English
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 17 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Analysis of essential histidine residues of maize branching enzymes by chemical modification and site-directed mutagenesis
AB Incubation of maize branching enzyme, mBEI and mBEII, with 100 μM diethylpyrocarbonate (DEPC) rapidly inactivated the enzymes. Treatment of the DEPC-inactivated enzymes with 100-500 mM hydroxylamine restored the enzyme activities. Spectroscopic data indicated that the inactivation of BE with DEPC was the result of histidine modification. The addition of the substrate amylose or amylopectin retarded the enzyme inactivation by DEPC, suggesting that the histidine residues are important

for substrate binding. In maize BEII, conserved histidine residues are in catalytic regions 1 (His320) and 4 (His508). His320 and His508 were individually replaced by Ala via site-directed mutagenesis to probe their role in catalysis. Expression of these mutants in E. coli showed a significant decrease of the activity and the mutant enzymes had Km values 10 times higher than the wild type. Therefore, residues His320 and His508 do play an important role in substrate binding.

AN 1998:784558 HCAPLUS <<LOGINID::20100610>>
DN 130:121357
TI Analysis of essential histidine residues of maize branching enzymes by chemical modification and site-directed mutagenesis
AU Funane, Kazumi; Libessart, Nathalie; Stewart, Douglas; Michishita, Toru; Preiss, Jack
CS Department of Biochemistry, Michigan State University, East Lansing, MI, 48824, USA
SO Journal of Protein Chemistry (1998), 17(7), 579-590
CODEN: JPCHD2; ISSN: 0277-8033
PB Plenum Publishing Corp.
DT Journal
LA English
OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)
RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 18 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Starch biosynthesis: understanding the functions and interactions of multiple isoenzymes of starch synthase and branching enzyme
AB A review with 47 refs. Starch is the most important source of calories on the planet and a vital storage compound in plants. Despite its importance, we do not fully understand how starch is synthesized, how starch synthesis is initiated and what controls starch structure. Many genes in the starch biosynthesis pathway have been isolated and multiple forms of starch synthase and branching enzyme have been identified. For example, five starch synthase genes and three branching enzyme genes have been cloned from maize. To fully illustrate the mechanism of starch biosynthesis, we need to understand the functions of individual enzyme as well as the concerted actions of multiple forms of enzymes in starch synthesis. Since maize is the number one supply of starch for food and non-food industries and also a good source for genetic and biochem. studies, here we will use maize as a model plant to discuss the mechanism of starch biosynthesis, particularly the initiation of starch synthesis, the functions and interaction of multiple isoenzymes of starch synthase and branching enzyme.
AN 1998:643789 HCAPLUS <<LOGINID::20100610>>
DN 130:48960
TI Starch biosynthesis: understanding the functions and interactions of multiple isoenzymes of starch synthase and branching enzyme
AU Guan, H. P.; Keeling, P. L.
CS ExSeed Genetics L. L. C. and Agronomy Department, Iowa State University, Ames, IA, 50011, USA
SO Trends in Glycoscience and Glycotechnology (1998), 10(54), 307-319
CODEN: TGGLEE; ISSN: 0915-7352
PB FCCA
DT Journal; General Review
LA English
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 19 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Genomic organization and promoter activity of the maize starch branching enzyme I gene
AB Starch branching enzymes (SBE) which catalyze the formation of α-1,6-glucan linkages are of crucial importance for the quantity and quality of starch synthesized in plants. In maize (Zea mays L.), three SBE isoforms (SBEI, IIa and IIb) have been identified and shown to exhibit differential expression patterns. As a first step toward understanding the regulatory mechanisms controlling their expression, the authors isolated and sequenced a maize genomic DNA (-2190 to +5929) which contains the entire coding region of SBEI (Sbe1) as well as 5'-and 3'-flanking sequences. Using this clone, the authors established a complete genomic organization of the maize Sbe1 gene. The transcribed region consists of 14 exons and 13 introns, distributed over 5.7 kb. A consensus TATA-box and a G-box containing a perfect palindromic sequence, CCACGTGG, were found in the 5'-flanking region. Genomic Southern blot anal. indicated that two Sbe1 genes with divergent 5'-flanking sequences exist in the maize genome, suggesting the possibility that they are differentially regulated. A chimeric construct containing the 5'-flanking region of Sbe1 (-2190 to +27) fused to the β-glucuronidase gene (pKG101) showed promoter activity after it was introduced into maize endosperm suspension cells by particle bombardment.
AN 1998:597027 HCAPLUS <<LOGINID::20100610>>
DN 129:311547
OREF 129:63465a,63468a
TI Genomic organization and promoter activity of the maize starch branching enzyme I gene
AU Kim, Kyung-Nam; Fisher, Dane K.; Gao, Ming; Guiltinan, Mark J.
CS Intercollege Graduate Programs in Plant Physiology and Genetics, Biotechnology Institute, Dep. Horticulture, Pennsylvania State University, Pennsylvania, PA, 16802, USA
SO Gene (1998), 216(2), 233-243
CODEN: GENED6; ISSN: 0378-1119
PB Elsevier Science B.V.
DT Journal
LA English
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 20 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Altering starch structure and functionality by manipulating expression of starch biosynthetic enzymes.
AB Starch functionality is a product of the fine structure of a given starch polymer. This structure is a result of the concerted action of several starch synthases, starch branching enzymes and starch debranching enzymes. To examine the relationship between starch polymer structure and starch functionality we are using transgenic approaches to control the expression of genes encoding starch biosynthetic enzymes and examine the impacts of altered gene expression on starch structure and functionality. We have isoalted and characterized maize cDNAs encoding Starch Branching Enzymes I and IIb (SBE I SBEIIb) and generated transgenic maize plants carrying constructions for under and over expression of these two genes. The effects of altered branching enzyme expression on starch polymer structure and starch functionality will be presented.
AN 1998:530122 HCAPLUS <<LOGINID::20100610>>
TI Altering starch structure and functionality by manipulating expression of

starch biosynthetic enzymes.
AU Lightner, Jonathan; Broglie, Karen; Cressman, Robert; Hines, Chris; Pearlstein, Rich; Hubbard, Natalie
CS Stine-Haskell Research Center, DuPont Agricultural Products, Newark, DE, 19714-0030, USA
SO Book of Abstracts, 216th ACS National Meeting, Boston, August 23-27 (1998), AGFD-137 Publisher: American Chemical Society, Washington, D. C.
CODEN: 66KYA2
DT Conference; Meeting Abstract
LA English

L8 ANSWER 21 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Heat-induced fragmentation of the maize waxy protein during protein extraction from starch granules
AB The starch granule of maize contains a characteristic set of tightly bound polypeptides. Granule-associated polypeptides are typically extracted from starch granules by heating starch granule suspensions at 90-100°C in a detergent such as SDS. Solubilized proteins are recovered by centrifugation and analyzed by gel electrophoresis. Previously identified tightly bound granule intrinsic proteins consist of the 85-kDa starch-branching enzyme IIb, the 76-kDa starch synthase I, and the 60-kD waxy (Wx) protein, also known as granule-bound starch synthase I. However, SDS exts. from starch granules of maize also contain a cluster of proteins ranging in mass between 47 and 32 kDa In this study, we analyzed this group of granule-associated proteins and found that each was recognized by the Wx antibody. A 15 amino acid N-terminal sequence from the 47-kDa polypeptide was identical to the predicted N-terminus of the Wx protein. Further anal. revealed that each immunoreactive polypeptide between 47 and 32 kDa was a heat-induced fragmentation product of the Wx protein. Conditions for the extraction of granule proteins were evaluated. Our results demonstrate that granule proteins are effectively released by mild extraction (10-rain incubation at 72°C). Relative to the Wx protein, starch synthase I and starch branching enzyme IIb were less susceptible to thermal fragmentation. These results demonstrate that the 85-, 76-, and 60-kDa polypeptides are authentic granule-intrinsic proteins, and that the majority of polypeptides between 47 and 32 kDa are artifacts of high-temperature granule extraction procedures.
AN 1998:485937 HCAPLUS <<LOGINID::20100610>>
DN 129:188502
OREF 129:38301a,38304a
TI Heat-induced fragmentation of the maize waxy protein during protein extraction from starch granules
AU Mu, Helen He; Mu-Forster, Chen; Bohonko, Monica; Wasserman, Bruce P.
CS Department of Food Science, New Jersey Agricultural Experiment Station, Cook College, Rutgers University, New Brunswick, NJ, HEAT-INDUCED FRAGMEN, USA
SO Cereal Chemistry (1998), 75(4), 480-483
CODEN: CECHAF; ISSN: 0009-0352
PB American Association of Cereal Chemists
DT Journal
LA English
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 22 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Starch granule-associated protein and transgenic plants producing starch with altered viscosity and phosphate content
AB Nucleic acid mols. are described encoding a starch granule-bound protein

from potato and maize as well as methods and recombinant DNA mols. for the production of transgenic plant cells and plants synthesizing a modified starch. Potato and maize cDNAs for a starch granule-associated protein were cloned and sequenced. Transgenic potatoes expressing an antisense version of the potato cDNA produced starch with .apprx.50% lower phosphate content and with altered gelling properties. When the starch granule-associated protein cDNA was expressed in Escherichia coli, glycogen with higher than normal phosphate content was produced.

AN 1998:424347 HCAPLUS <<LOGINID::20100610>>
DN 129:91420
OREF 129:18743a,18746a
TI Starch granule-associated protein and transgenic plants producing starch with altered viscosity and phosphate content
IN Kossmann, Jens; Emmermann, Michael
PA Planttec Biotechnologie G.m.b.H., Germany
SO PCT Int. Appl., 123 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

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PI	WO 9827212	A1	19980625	WO 1997-EP7123	19971218	<--
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW					
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG					
	DE 19653176	A1	19980625	DE 1996-19653176	19961219	<--
	CA 2272844	A1	19980625	CA 1997-2272844	19971218	<--
	AU 9858577	A	19980715	AU 1998-58577	19971218	<--
	AU 740492	B2	20011108			
	EP 950107	A1	19991020	EP 1997-954424	19971218	<--
	EP 950107	B1	20070321			
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, NL, SE, PT					
	JP 2001522223	T	20011113	JP 1998-527334	19971218	<--
	JP 4098365	B2	20080611			
	AT 357522	T	20070415	AT 1997-954424	19971218	<--
	PT 950107	E	20070531	PT 1997-954424	19971218	<--
	ES 2280086	T3	20070901	ES 1997-954424	19971218	<--
	US 7186898	B1	20070306	US 1999-334103	19990616	<--
PRAI	DE 1996-19653176	A	19961219	<--		
	WO 1997-EP7123	W	19971218	<--		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 23 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Characterization of the difference of starch branching enzyme activities in normal and low-amylopectin maize during kernel development
AB In order to determine the reasons for the differences in structure between starch from a normal and a low-amylopectin maize variety, the activities of all the enzymes in the committed pathway of starch synthesis were studied throughout kernel development. Levels of ADP glucose pyrophosphorylase and starch synthase activity were found to be broadly similar between the two varieties but the low-amylopectin starch (LAPS)

maize variety showed dramatically reduced starch branching enzyme activity, with an almost total absence of the branching enzyme II isoform. SEM showed a significant alteration in the morphol. of the starch granules of the low-amylopectin maize. The results suggest that the increased amylose and the reduction of high mol. weight amylopectin in the LAPS starch results from the absence of the branching enzyme II isoform. This evidence suggests that the different branching enzyme isoforms contribute sep. to the synthesis and final structure of amylopectin.

AN 1998:418224 HCAPLUS <<LOGINID::20100610>>
DN 129:186465
OREF 129:37801a,37804a
TI Characterization of the difference of starch branching enzyme activities in normal and low-amylopectin maize during kernel development
AU Sidebottom, C.; Kirkland, M.; Strongitharm, B.; Jeffcoat, R.
CS Biosciences Division, Unilever Research, Bedford, MK44 1LQ, UK
SO Journal of Cereal Science (1998), 27(3), 279-287
CODEN: JCSCDA; ISSN: 0733-5210
PB Academic Press Ltd.
DT Journal
LA English
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 24 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Surface localization of zein storage proteins in starch granules from maize endosperm. Proteolytic removal by thermolysin and in vitro crosslinking of granule-associated polypeptides
AB Starch granules from maize (Zea mays) contain a characteristic group of polypeptides that are tightly associated with the starch matrix (C. Mu-Forster, et al ,1996). Zeins comprise about 50% of the granule-associated proteins, and their spatial distribution within the starch granule was determined Proteolysis of starch granules at subgelatinization temps. using the thermophilic protease thermolysin led to selective removal of the zeins, whereas granule-associated proteins of 32 kD or above, including the waxy protein, starch synthase I, and starch-branching enzyme IIb, remained refractory to proteolysis. Granule-associated proteins from maize are therefore composed of two distinct classes, the surface-localized zeins of 10 to 27 kD and the granule-intrinsic proteins of 32 kD or higher. The origin of surface-localized δ-zein was probed by comparing δ-zein levels of starch granules obtained from homogenized whole endosperm with granules isolated from amyloplasts. Starch granules from amyloplasts contained markedly lower levels of δ-zein relative to granules prepared from whole endosperm, thus indicating that δ-zein adheres to granule surfaces after disruption of the amyloplast envelope. Crosslinking expts. show that the zeins are deposited on the granule surface as aggregates. In contrast, the granule-intrinsic proteins are prone to covalent modification, but do not form intermol. cross-links. Thus, individual granule intrinsic proteins exist as monomers and are not deposited in the form of multimeric clusters within the starch matrix.
AN 1998:258959 HCAPLUS <<LOGINID::20100610>>
DN 129:2723
OREF 129:667a,670a
TI Surface localization of zein storage proteins in starch granules from maize endosperm. Proteolytic removal by thermolysin and in vitro crosslinking of granule-associated polypeptides
AU Mu-Forster, Chen; Wasserman, Bruce P.
CS Department of Food Science Cook College, New Jersey Agricultural

Experiment Station, Rutgers University, New Brunswick, NJ, 08901-8520, USA
SO Plant Physiology (1998), 116(4), 1563-1571
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 25 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Polypeptides of the maize amyloplast stroma. Stromal localization of starch-biosynthetic enzymes and identification of an 81-kilodalton amyloplast stromal heat-shock cognate
AB In the developing endosperm of monocotyledonous plants, starch granules are synthesized and deposited within the amyloplast. A soluble stromal fraction was isolated from amyloplasts of immature maize (Zea mays L.) endosperm and analyzed for enzyme activities and polypeptide content. Specific activities of starch synthase and starch-branching enzyme (SBE), but not the cytosolic marker alc. dehydrogenase, were strongly enhanced in soluble amyloplast stromal fractions relative to soluble exts. obtained from homogenized kernels or endosperms. Immunoblot anal. demonstrated that starch synthase 1, SBEIIb, and sugary1, the putative starch-debranching enzyme, were each highly enriched in the amyloplast stroma, providing direct evidence for the localization of starch-biosynthetic enzymes within this compartment. Anal. of maize mutants shows the deficiency of the 85-kD SBEIIb polypeptide in the stroma of amylose extender cultivars and that the dull mutant lacks a >220-kD stromal polypeptide. The stromal fraction is distinguished by differential enrichment of a characteristic group of previously undocumented polypeptides. N-terminal sequence anal. revealed that an abundant 81-kD stromal polypeptide is a member of the Hsp70 family of stress-related proteins. Moreover, the 81-kD stromal polypeptide is strongly recognized by antibodies specific for an Hsp70 of the chloroplast stroma. These findings are discussed in light of implications for the correct folding and assembly of soluble, partially soluble, and granule-bound starch-biosynthetic enzymes during import into the amyloplast.
AN 1998:258947 HCAPLUS <<LOGINID::20100610>>
DN 129:2721
OREF 129:667a,670a
TI Polypeptides of the maize amyloplast stroma. Stromal localization of starch-biosynthetic enzymes and identification of an 81-kilodalton amyloplast stromal heat-shock cognate
AU Yu, Ying; Mu, Helen He; Mu-Forster, Chen; Wasserman, Bruce P.
CS Department of Food Science Cook College, New Jersey Agricultural Experiment Station Rutgers University, New Brunswick, NJ, 08901-8520, USA
SO Plant Physiology (1998), 116(4), 1451-1460
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
OSC.G 19 THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 26 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Promoter of wheat wbeI gene for expressing foreign genes in monocotyledonous plants
AB A DNA fragment for directing the expression of foreign or endogenous genes or RNA in cells of monocot plants. The fragment comprises a sequence

corresponding to a first part of a putative type I starch branching enzyme gene (wbeI) present in wheat and a 5'-region upstream of the gene, or a part of the sequence that is effective for increasing the expression of the foreign or endogenous gene in the plant cells. The indicated sequence contains two promoter regions, P1 and P2. A DNA fragment effective to increase expression comprises at least one of the promoter regions, or an effective part. The fragment can be obtained from a genomic library of wheat and can be fused to suitable genes and markers and inserted into suitable vectors for expression in transgenic monocot plants. The P2 promoter, found in the second intron, was 2-4 times more active in wheat, barley, oat and maize cells that the P1-P2 combination.

AN 1998:256690 HCAPLUS <<LOGINID::20100610>>
DN 128:253799
OREF 128:50155a,50158a
TI Promoter of wheat wbeI gene for expressing foreign genes in monocotyledonous plants
IN Baga, Monica; Chibbar, Ravindra N.; Kartha, Kutty K.
PA Baga, Monica, Can.; Chibbar, Ravindra N.; Kartha, Kutty K.
SO Can. Pat. Appl., 78 pp.
CODEN: CPXXEB
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	CA 2196834	A1	19971204	CA 1997-2196834	19970205 <--
	US 5866793	A	19990202	US 1996-773251	19961223 <--
PRAI	CA 1996-2178016	A	19960603 <--		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)

L8 ANSWER 27 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Characterization of dull1, a maize gene coding for a novel starch synthase
AB The maize dull1 (du1) gene is a determinant of the structure of endosperm starch, and du1-mutations affect the activity of two enzymes involved in starch biosynthesis, starch synthase II (SSII) and starch branching enzyme IIa (SBEIIa). Six novel du1-mutations generated in Mutator-active plants were identified. A portion of the du1 locus was cloned by transposon tagging, and a nearly full-length Du1 cDNA sequence was determined Du1 codes for a predicted 1674-residue protein, comprising one portion that is similar to SSIII of potato, as well as a large unique region. Du1 transcripts are present in the endosperm during the time of starch biosynthesis, but the mRNA was undetectable in leaf or root tissue. The predicted size of the Du1 gene product and its expression pattern are consistent with those of maize SSII. The Du1 gene product contains two repeated regions in its unique N terminus. One of these contains a sequence identical to a conserved segment of SBEs. We conclude that Du1 codes for a starch synthase, most likely SSII, and that secondary effects of du1-mutations, such as reduction of SBEIIa, result from the primary deficiency in this starch synthase.
AN 1998:215485 HCAPLUS <<LOGINID::20100610>>
DN 129:2125
OREF 129:531a,534a
TI Characterization of dull1, a maize gene coding for a novel starch synthase
AU Gao, Ming; Wanat, Jennifer; Stinard, Philip S.; James, Martha G.; Myers, Alan M.
CS Department of Biochemistry and Biophysics, Iowa State University, Ames,

IA, 50011, USA
SO Plant Cell (1998), 10(3), 399-412
CODEN: PLCEEW; ISSN: 1040-4651
PB American Society of Plant Physiologists
DT Journal
LA English
OSC.G 100 THERE ARE 100 CAPLUS RECORDS THAT CITE THIS RECORD (100 CITINGS)
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 28 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Linkage mapping of starch branching enzyme
III in rice (Oryza sativa L.) and prediction of location of orthologous genes in other grasses
AB The chromosomal position of Starch Branching
Enzyme III (SBEIII) was determined via linkage to RFLP markers on an existing mol. map of rice (Oryza sativa L.). A cDNA of 890 bp was generated using specific PCR primers designed from available SBEIII sequence data and used as a probe in Southern anal. The SBEIII cDNA hybridized to multiple restriction fragments, but these fragments mapped to a single locus on rice chromosome 2, flanked by CDO718 and RG157. The detection of a multiple-copy hybridization pattern suggested the possibility of a tandemly duplicated gene at this locus. The map location of orthologous SBE genes in maize, wheat, and oat were predicted based on previously published genetic studies and comparative maps of the grass family.
AN 1997:370751 HCAPLUS <<LOGINID::20100610>>
DN 127:14031
OREF 127:2763a,2766a
TI Linkage mapping of starch branching enzyme
III in rice (Oryza sativa L.) and prediction of location of orthologous genes in other grasses
AU Harrington, S. E.; Bligh, H. F. J.; Park, W. D.; Jones, C. A.; McCouch, S. R.
CS Development Plant Breeding Biometry, Cornell University, Ithaca, NY, 14853-1902, USA
SO Theoretical and Applied Genetics (1997), 94(5), 564-568
CODEN: THAGA6; ISSN: 0040-5752
PB Springer
DT Journal
LA English
OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (22 CITINGS)
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 29 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Comparing the properties of Escherichia coli branching enzyme and maize branching enzyme
AB Escherichia coli glycogen branching enzyme (GBE) and
maize starch branching enzymes I (SBEI) and II (SBEII)
were expressed in E. coli and purified. E. coli GBE branched amylose at a higher rate than did SBEII, but branched amylose at a lower rate than did SBEI. Similar to SBEI, GBE branched amylopectin at a lower rate than did SBEII. High-performance anion-exchange chromatog. anal. of the branched products produced by BE revealed the min. chain length (cl) required for branching. While GBE and SBEII showed the same min. cl [d.p. (dp) 12] required for branching, SBEI had a slightly higher min. cl (dp 16) requirement for branching. The major differences between GBE and SBE are their specificities in terms of the size of chains transferred. In comparison with SBE, GBE had a much narrower size range of chains transferred and transferred mainly shorter chains. While SBEI and SBEII

produced a large number of chains ranging from dp 6 to over dp 30, GBE predominantly transferred chains ranging from dp 5 to 16 and produced only a very small number of long chains with dp greater than 20. Although it has been reported that SBEI and SBEII preferentially transfer longer and shorter chains, resp. (1), this study further defines the differences between SBEI and SBEII in the size of chains transferred. SBEI predominantly transfers longer chains with dp greater than 10, while producing few shorter chains with dp 3 to 5. In contrast, SBEII preferentially transfers smaller chains with dp 3 to 9, with the most abundant chains being dp 6 and 7. The significance of min. chain-length requirement by SBE is discussed in setting the invariant size of amylopectin cluster size (9 nm).

AN 1997:347385 HCAPLUS <<LOGINID::20100610>>
DN 127:46831
OREF 127:8835a,8838a
TI Comparing the properties of Escherichia coli branching enzyme and maize branching enzyme
AU Guan, Hanping; Li, Ping; Imparl-Radosevich, Jennifer; Preiss, Jack; Keeling, Peter
CS ExSeed Genetics, Agronomy Dep., Iowa State Univ., Ames, IA, 50011, USA
SO Archives of Biochemistry and Biophysics (1997), 342(1), 92-98
CODEN: ABBIA4; ISSN: 0003-9861
PB Academic
DT Journal
LA English
OSC.G 43 THERE ARE 43 CAPLUS RECORDS THAT CITE THIS RECORD (43 CITINGS)
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 30 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Independent genetic control of maize starch-branching enzymes IIa and IIb. Isolation and characterization of a Sbe2a cDNA
AB In maize (Zea mays L.) three isoforms of starch-branching enzyme (SBEI, SBEIIa, and SBEIIb) are involved in the synthesis of amylopectin, the branched component of starch. To isolate a cDNA encoding SBEIIa, degenerate oligonucleotides based on domains highly conserved in Sbe2 family members were used to amplify Sbe2-family cDNA from tissues lacking SBEIIb activity. The predicted amino acid sequence of a Sbe2a cDNA matches the N-terminal sequence of SBEIIa protein purified from maize endosperm. The size of the mature protein deduced from the cDNA also matches that of SBEIIa. Features of the predicted protein are most similar to members of the SBEII family; however, it differs from maize SBEIIb in having a 49-amino acid N-terminal extension and a region of substantial sequence divergence. Sbe2a mRNA levels are 10-fold higher in embryonic than in endosperm tissue, and are much lower than Sbe2b in both tissues. Unlike Sbe2b, Sbe2a-hybridizing mRNA accumulates in leaf and other vegetative tissues, consistent with the known distribution of SBEIIa and SBEIIb activities.

AN 1997:332511 HCAPLUS <<LOGINID::20100610>>
DN 127:76709
OREF 127:14545a,14548a
TI Independent genetic control of maize starch-branching enzymes IIa and IIb. Isolation and characterization of a Sbe2a cDNA
AU Gao, Ming; Fisher, Dane K.; Kim, Kyung-Nam; Shannon, Jack C.; Guiltinan, Mark J.
CS Biotechnology Inst., Pennsylvania State Univ., University Park, PA, 16802, USA
SO Plant Physiology (1997), 114(1), 69-78
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists

DT Journal
LA English
OSC.G 56 THERE ARE 56 CAPLUS RECORDS THAT CITE THIS RECORD (56 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 31 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat
AB A full-length cDNA (2970 bp) encoding a starch branching enzyme II (SBEII; EC 2.4.1.18) in wheat (Triticum aestivum L. cv Fielder) kernel was isolated from a cDNA library. The translated region of the cDNA predicted a 823 amino acid primary product with a mol. mass of 91.4 kDa. A 54 amino acid transit peptide was postulated to be cleaved from the pre-protein to give a 769 amino acid (85.4 kDa) mature polypeptide, which showed extensive sequence similarity to SBEII sequences characterized from maize, rice and pea. Expression of the isolated cDNA in a BE-deficient E. coli strain demonstrated that it encoded a functional BE. RNA anal. of Sbe2 gene expression during seed development revealed that Sbe2 mRNA levels were highest in young kernels (5-10 days post-anthesis) and declined as the kernels matured.
AN 1997:123840 HCAPLUS <<LOGINID::20100610>>
DN 126:248817
OREF 126:48055a,48058a
TI Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat
AU Nair, Ramesh B.; Baga, Monica; Scoles, Graham J.; Kartha, Kutty K.; Chibbar, Ravindra N.
CS Department of Crop Science and Plant Ecology, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Can.
SO Plant Science (Shannon, Ireland) (1997), 122(2), 153-163
CODEN: PLSCE4; ISSN: 0168-9452
PB Elsevier
DT Journal
LA English
OSC.G 30 THERE ARE 30 CAPLUS RECORDS THAT CITE THIS RECORD (30 CITINGS)

L8 ANSWER 32 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Molecular characterization of starch branching enzyme genes, sbe1, sbe2b and sbe2a in maize (Zea mays L.)
AB Unavailable
AN 1997:95523 HCAPLUS <<LOGINID::20100610>>
DN 126:115703
OREF 126:22309a,22312a
TI Molecular characterization of starch branching enzyme genes, sbe1, sbe2b and sbe2a in maize (Zea mays L.)
AU Gao, Ming
CS Pennsylvania State Univ., University Park, PA, USA
SO (1996) 108 pp. Avail.: Univ. Microfilms Int., Order No. DA9702296
From: Diss. Abstr. Int., B 1997, 57(8), 4919
DT Dissertation
LA English

L8 ANSWER 33 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Differential expression and properties of starch-branching enzyme isoforms in developing wheat endosperm
AB Three forms of starch-branching enzyme (BE) from developing hexaploid wheat (Triticum aestivum) endosperm have been

partially purified and characterized. Immunol. cross-reactivities indicate that two forms (WBE-IAD, 88 kDa, and WBE-IB, 87 kDa) are related to the maize BE I class and that WBE-II (88 kDa) is related to maize BE II. Comparison of the N-terminal sequences from WBE-IAD and WBE-II with maize and rice BEs confirms these relationships. Evidence is presented from the anal. of nullisomic-tetrasomic wheat lines demonstrating that WBE-IB is located on chromosome 7B and that the WBE-IAD fraction contains polypeptides that are encoded on chromosomes 7A and 7D. The wheat endosperm BE classes are differentially expressed during endosperm development. WBE-II is expressed at a constant level throughout mid and late endosperm development. In contrast, WBE-IAD and WBE-IB are preferentially expressed in late endosperm development. Differences are also observed in the kinetic characteristics of the enzymes. The WBE-I isoforms have a 2- to 5-fold higher affinity for amylose than does WBE-II, and the WBE-I isoforms are activated up to 5-fold by phosphorylated intermediates and inorg. phosphate, whereas WBE-II is activated only 50%. The potential implications of this activation of BE I for starch biosynthesis are discussed.

AN 1997:73618 HCAPLUS <<LOGINID::20100610>>
DN 126:169149
OREF 126:32649a,32652a
TI Differential expression and properties of starch-branching enzyme isoforms in developing wheat endosperm
AU Morell, Matthew K.; Blennow, Andreas; Kosar-Hashemi, Behjat; Samuel, Michael S.
CS Cooperative Res. Cent. Plant Sci., Canberra, ACT 2601, Australia
SO Plant Physiology (1997), 113(1), 201-208
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
OSC.G 90 THERE ARE 90 CAPLUS RECORDS THAT CITE THIS RECORD (90 CITINGS)

L8 ANSWER 34 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Evolutionary conservation and expression patterns of maize starch branching enzyme I and IIb genes suggest isoform specialization
AB Expression of the maize (Zea mays L.) starch branching enzyme (SBE) genes Sbe1 and Sbe2 were characterized during kernel development and in vegetative tissues. The onset of Sbe1 and Sbe2 expression during endosperm development was similar to that of other genes involved in starch biosynthesis (Wx, Sh2 and Bt2). However, the expression of Sbe2 peaked earlier than that of Sbe1 in developing endosperm and embryos resulting in a shift in the ratio of Sbe1 to Sbe2 relative message levels during kernel and embryo development. Transcripts hybridizing to the Sbe2 probe were not detectable in leaves kernel and embryo development. Transcripts hybridizing to the Sbe2 probe were not detectable in leaves or roots which nonetheless have SBEII enzymic activity, suggesting that there may be another divergent SBEII-like gene(s) in maize. A similar expression pattern is shared between the maize genes and related genes in pea, which together with their evolutionary conservation, suggests that the SBE isoforms may play unique roles in starch biosynthesis during plant development.
AN 1996:466120 HCAPLUS <<LOGINID::20100610>>
DN 125:137991
OREF 125:25725a
TI Evolutionary conservation and expression patterns of maize starch branching enzyme I and IIb genes suggest isoform specialization
AU Gao, Ming; Fisher, Dane K.; Kim, Kyung-Nam; Shannon, Jack C.; Guiltinan,

Mark J.
CS Dep. of Horticulture, Pennsylvania State Univ., University Park, PA, 16802, USA
SO Plant Molecular Biology (1996), 30(6), 1223-1232
CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer
DT Journal
LA English
OSC.G 52 THERE ARE 52 CAPLUS RECORDS THAT CITE THIS RECORD (52 CITINGS)

L8 ANSWER 35 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Physical association of starch biosynthetic enzymes with starch granules of maize endosperm. Granule-associated forms of starch synthase I and starch branching enzyme II
AB Antibodies were used to probe the degree of association of starch biosynthetic enzymes with starch granules isolated from maize (Zea mays) endosperm. Graded washings of the starch granule, followed by release of polypeptides by gelatinization in 2% sodium dodecyl sulfate, enables distinction between strongly and loosely adherent proteins. Mild aqueous washing of granules resulted in near-complete solubilization of ADP-glucose pyrophospyorylase, indicating that little, if any, ADP-glucose pyrophosphorylase is granule associated In contrast, all of the waxy protein plus significant levels of starch synthase I and starch branching enzyme II (BEII) remained granule associated Stringent washings using protease and detergent demonstrated that the waxy protein, more than 85% of total endosperm starch synthase I protein, and more than 45% of BEII protein were strongly associated with starch granules. Rates of polypeptide accumulation within starch granules remained constant during endosperm development. Soluble and granule-derived forms of BEII yielded identical peptide maps and overlapping tryptic fragments closely aligned with deduced amino acid sequences from BEII cDNA clones. These observations provide direct evidence that BEII exists as both soluble and granule-associated entities. Thus, it is concluded that each of the known starch biosynthetic enzymes in maize endosperm exhibits a differential propensity to associate with, or to become irreversibly entrapped within, the starch granule.
AN 1996:436720 HCAPLUS <<LOGINID::20100610>>
DN 125:81944
OREF 125:15407a,15410a
TI Physical association of starch biosynthetic enzymes with starch granules of maize endosperm. Granule-associated forms of starch synthase I and starch branching enzyme II
AU Mu-Forster, Chen; Huang, Rongmin; Powers, Joseph R.; Harriman, Robert W.; Knight, Mary; Singletary, George W.; Keeling, Peter L.; Wasserman, Bruce P.
CS Dep. Food Sci., Rutgers Univ., New Brunswick, NJ, 08903-0231, USA
SO Plant Physiology (1996), 111(3), 821-829
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
OSC.G 82 THERE ARE 82 CAPLUS RECORDS THAT CITE THIS RECORD (82 CITINGS)

L8 ANSWER 36 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Two closely related cDNAs encoding starch branching enzyme from Arabidopsis thaliana
AB Two starch branching enzyme (SBE) cDNAs were identified in an Arabidopsis seedling hypocotyl library using maize Sbe1 and Sbe2 cDNAs as probes. The two cDNAs have diverged 5', and 3' ends, but encode proteins which share 90% identity over an extensive region with 70% identity to maize SBE IIb. Genomic

Southern blots suggest that the two cDNAs are the products of single, independent genes, and that addn1., more distantly related SBE genes may exist in the Arabidopsis genome. The two cDNAs hybridize to transcripts which show similar expression patterns in Arabidopsis vegetative and reproductive tissues, including seedlings, inflorescence rachis, mature leaves, and flowers. This is the first report of the identification of cDNAs encoding two closely related starch branching enzymes from the same species.

AN 1996:149142 HCAPLUS <<LOGINID::20100610>>
DN 124:224561
OREF 124:41433a,41436a
TI Two closely related cDNAs encoding starch branching enzyme from Arabidopsis thaliana
AU Fisher, Dane K.; Gao, Ming; Kim, Kyung-Nam; Boyer, Charles D.; Guiltinan, Mark J.
CS Dep. Horticulture, Pennsylvania State Univ., Univ. Park, PA, 16802, USA
SO Plant Molecular Biology (1996), 30(1), 97-108
CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer
DT Journal
LA English
OSC.G 27 THERE ARE 27 CAPLUS RECORDS THAT CITE THIS RECORD (27 CITINGS)

L8 ANSWER 37 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Allelic analysis of the maize amylose-extender locus suggests that independent genes encode starch-branching enzymes IIa and IIb
AB Starch branching enzymes (SBE) catalyze the formation of α-1,6-glucan linkages in the biosynthesis of starch. Three distinct SBE isoforms have been identified in maize (Zea mays L.) endosperm, SBEI, Iia, and IIb. Independent genes have been identified that encode maize SBEI and IIb; however, it has remained controversial as to whether SBEIIa and IIb result from post-transcriptional processes acting on the product of a single gene or whether they are encoded by sep. genes. Thus, 16-isogenic lines carrying independent alleles of the maize amylose-extender (ae) locus, the structural gene for SBEIIb, were analyzed. At 22 days after pollination ae-B1 endosperm expressed little She2b (ae)-hybridizing transcript, and as expected, ae-B1 endosperm also lacked detectable SBEIIb enzymic activity,. Also, ae-B1 endosperm contained SBEIIa enzymic activity, strongly supporting the hypothesis that endosperm SBEIIa and IIb are encoded by sep. genes. Furthermore, addition to encoding the predominant Sbe2b-hybridizing message expressed in endosperm, the ae gene also encodes the major She2b-like transcript expressed in developing embryos and tassels.

AN 1996:119513 HCAPLUS <<LOGINID::20100610>>
DN 124:170828
OREF 124:31587a,31590a
TI Allelic analysis of the maize amylose-extender locus suggests that independent genes encode starch-branching enzymes IIa and IIb
AU Fisher, Dane K.; Gao, Ming; Kim, Kyung-Nam; Boyer, Charles D.; Guiltinan, Mark J.
CS Biotechnol. Inst., Pennsylvania State Univ., University Park, PA, 16802, USA
SO Plant Physiology (1996), 110(2), 611-19
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
OSC.G 39 THERE ARE 39 CAPLUS RECORDS THAT CITE THIS RECORD (39 CITINGS)

L8 ANSWER 38 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Molecular genetic analysis of multiple isoforms of starch branching enzyme with emphasis on Zea mays L. (Arabidopsis thaliana)
AB Unavailable
AN 1996:103412 HCAPLUS <<LOGINID::20100610>>
DN 124:166805
OREF 124:30743a,30746a
TI Molecular genetic analysis of multiple isoforms of starch branching enzyme with emphasis on Zea mays L. (Arabidopsis thaliana)
AU Fisher, Dane Kinard
CS Pennsylvania State Univ., University Park, PA, USA
SO (1995) 185 pp. Avail.: Univ. Microfilms Int., Order No. DA9600172
From: Diss. Abstr. Int., B 1995, 56(9), 4707
DT Dissertation
LA English

L8 ANSWER 39 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Bt1, a structural gene for the major 39-44 kDa amyloplast membrane polypeptides
AB The relationship between the Bt1 gene (Bt1) and the major 39-44 kDa amyloplast membrane polypeptides which were deficient in amyloplast membranes of brittle1 (bt1) kernels of maize (Zea mays L.) was examined A rapid yet gentle procedure for the isolation of amyloplasts from immature kernels is described. These amyloplasts were relatively free of contamination by other cellular components, and immunol. studies showed that they contained polypeptides which reacted with antibodies to maize starch branching enzyme and ADP-Glc pyrophosphorylase. Purified membranes isolated from the amyloplast contained a polypeptide which reacted with antibodies to the Pi-translocator from spinach chloroplasts. However, a cluster of 39-44 kDa polypeptides accounted for about 40% of the total amyloplast membrane protein from W64A kernels. These polypeptides were specifically recognized by antibodies raised against a fusion protein consisting of 56 amino acids of the carboxyl terminus of the BT1 protein and glutathione S-transferase. The BT1 antibodies also reacted with the abundant polypeptides in amyloplast membranes from hybrid kernels (Doebler 66XP and Pioneer 3780), and the shrunken1 and shrunken2 mutant genotypes, but no BT1 reacting polypeptides were present in amyloplast membranes from bt1 mutant kernels. BT1 was detected by the immunoblot procedure in microsomal membranes from embryo and pericarp tissues from the kernel, from seedling roots and shoots, or in membranes from mitochondria and chloroplasts. The same BT1 immunoblot pattern was obtained for proteins extracted from microsomal membranes from developing endosperm and from purified amyloplast membranes. A linear relationship between the number of copies of Bt1 alleles and the levels of BT1 in endosperm microsomal membranes was demonstrated in a gene dosage series. BT1 was not extracted from amyloplast membranes by chloroform/methanol or by alkaline buffer at pH 11.5, but was partially extracted by 0.1 M NaOH. Thus, Bt1 is the structural gene for the major 39-44 kDa amyloplast membrane polypeptides and these polypeptides are integral proteins specific to amyloplast membranes from the endosperm.
AN 1996:20003 HCAPLUS <<LOGINID::20100610>>
DN 124:50872
OREF 124:9531a,9534a
TI Bt1, a structural gene for the major 39-44 kDa amyloplast membrane polypeptides
AU Cao, Heping; Sullivan, Thomas D.; Boyer, Charles D.; Shannon, Jack C.
CS Dept Biochemistry, Michigan State Univ., East Lansing, MI, 48824, USA
SO Physiologia Plantarum (1995), 95(2), 176-86

CODEN: PHPLAI; ISSN: 0031-9317
PB Munksgaard
DT Journal
LA English
OSC.G 39 THERE ARE 39 CAPLUS RECORDS THAT CITE THIS RECORD (39 CITINGS)

L8 ANSWER 40 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI A cDNA encoding starch branching enzyme I from maize endosperm
AB An apparently full-length cDNA for starch branching enzyme (EC 2.4.1.18) isoform I was isolated by screening with a PCR fragment derived from primers based on a previously isolated cDNA clone. The open reading frame codes for 822 amino acids, including a putative 63-amino acid transit peptide.
AN 1995:695609 HCAPLUS <<LOGINID::20100610>>
DN 123:162340
OREF 123:28731a,28734a
TI A cDNA encoding starch branching enzyme I from maize endosperm
AU Fisher, Dane K.; Kim, Kyung-Nam; Gao, Ming; Boyer, Charles D.; Guiltinan, Mark J.
CS Dep. Horticulture, Pennsylvania State Univ., University Park, PA, 16802, USA
SO Plant Physiology (1995), 108(3), 1313-14
CODEN: PLPHAY; ISSN: 0032-0889
PB Dekker
DT Journal
LA English
OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (22 CITINGS)

L8 ANSWER 41 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Effect of temperature on enzymes in the pathway of starch biosynthesis in developing wheat and maize grain
AB Soluble starch synthase (SSS) is shown to be a major site of control of flux through the pathway of starch synthesis in developing wheat and maize grain. Temps. above 25°C adversely affect flux, and therefore, limit yield. This process is linked to SSS which is heat sensitive. Two apparently different properties of SSS can be identified which differ in the period required before full activity is restored after heat treatment. First, enzyme rate is adversely affected by elevated temperature, an effect which is reversible on returning to a lower temperature The effect on enzyme rate was quantified using enzyme Q10 which was found to begin to be sub-optimal above 20°. Second, with a prolonged period of exposure to elevated temperature there is a loss of enzyme activity which is not freely reversible which we have termed thermal inactivation. Although this occurs at temps. in excess of 20° in wheat, higher temps. of more than 30° are needed in maize SSS. Elevated temperature did not affect the inherent stability or Q10 characteristics of other enzymes in the pathway of starch synthesis except for branching enzyme which might have minimal flux-control strength. SSS thermal inactivation may not be a major problem in field conditions for developing maize grain, because temps. rarely are high enough. However, it is suggested that the effect on enzyme Q10 is more physiol. relevant, since maize SSS is operating sub-optimally as temps. exceed 20°. Calcns. of the redns. in maize US corn-belt yield showed that significant yield improvement might be obtained by a 5° shift in the temperature optimum. Thus, selections for a more temperature tolerant form of maize SSS were conducted using enzyme Q10 as a selection tool. Of several hundred maize specimens screened, two were found to be significantly

different. However, attempts to use backcross breeding to transfer this trait from the tropical donor to another line have not yet succeeded.
AN 1995:473988 HCAPLUS <<LOGINID::20100610>>
DN 122:286717
OREF 122:52151a,52154a
TI Effect of temperature on enzymes in the pathway of starch biosynthesis in developing wheat and maize grain
AU Keeling, P. L.; Banisadr, R.; Barone, L.; Wasserman, B. P.; Singletary, G. W.
CS Applied Biology Project, ICI Seeds, Slater, IA, 50244, USA
SO Australian Journal of Plant Physiology (1994), 21(6), 807-27
CODEN: AJPPCH; ISSN: 0310-7841
PB Commonwealth Scientific and Industrial Research Organization
DT Journal
LA English
OSC.G 28 THERE ARE 28 CAPLUS RECORDS THAT CITE THIS RECORD (28 CITINGS)

L8 ANSWER 42 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Starch branching enzymes belonging to distinct enzyme families are differentially expressed during pea embryo development
AB CDNA clones for two isoforms of starch branching enzyme (SBEI and SBEII) have been isolated from pea embryos and sequenced. The deduced amino acid sequences of pea SBEI and SBEII are closely related to starch branching enzymes of maize, rice, potato and cassava and a number of glycogen branching enzymes from yeast, mammals and several prokaryotic species. In comparison with SBEI, the deduced amino acid sequence of SBEII lacks a flexible domain at the N-terminus of the mature protein. This domain is also present in maize SBEII and rice SBEIII and resembles one previously reported for pea granule-bound starch synthase II (GBSSII). However, in each case it is missing from the other isoform of SBE from the same species. On the basis of this structural feature (which exists in some isoforms from both monocots and dicots) and other differences in sequence, SBEs from plants may be divided into two distinct enzyme families. There is strong evidence from our own and other work that the amylopectin products of the enzymes from these two families are qual. different. Pea SBEI and SBEII are differentially expressed during embryo development. SBEI is relatively highly expressed in young embryos while maximum expression of SBEII occurs in older embryos. The differential expression of isoforms which have distinct catalytic properties means that the contribution of each SBE isoform to starch biosynthesis changes during embryo development. Qual. measurement of amylopectin from developing and maturing embryos confirms that the nature of amylopectin changes during pea embryo development and that this correlates with the differential expression of SBE isoforms.
AN 1995:459734 HCAPLUS <<LOGINID::20100610>>
DN 123:136225
OREF 123:24081a,24084a
TI Starch branching enzymes belonging to distinct enzyme families are differentially expressed during pea embryo development
AU Burton, Rachel A.; Bewley, J. Derek; Smith, Alison M.; Bhattacharyya, Madan K.; Tatge, Helma; Ring, Steve; Bull, Vicky; Hamilton, William D. O.; Martin, Cathie
CS John Innes Centre, John Innes Institute, Norwich, NR4 7UH, UK
SO Plant Journal (1995), 7(1), 3-15
CODEN: PLJUED; ISSN: 0960-7412
DT Journal
LA English
OSC.G 91 THERE ARE 91 CAPLUS RECORDS THAT CITE THIS RECORD (91 CITINGS)

L8 ANSWER 43 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Expression of branching enzyme II of maize endosperm in Escherichia coli
AB A cDNA clone encoding maize branching enzyme II (BEII) has been independently isolated from a maize endosperm cDNA library. The deduced protein sequence of maize BEII was compared with that of BE from diverse sources. The gene encoding mature BEII of maize endosperm has been expressed in E. coli using the T7 promoter. The expressed BEII was purified to near homogeneity so that amylolytic activity and bacterial BE could be completely eliminated from the BE preparation The expressed enzyme showed very similar properties to those of bEII purified from developing maize endosperm. This result confirmed our earlier report that BEII had a lower rate of branching amylose and the rate of branching amylopectin was twice that of branching amylose. This study also showed a greater advantage of purifying BEII from the bacterial expression system than from developing maize endosperm. Most importantly, this study has established a useful tool to study the structure-function relationships of the maize BE using site-directed mutagenesis.
AN 1995:140589 HCAPLUS <<LOGINID::20100610>>
DN 123:4386
OREF 123:915a,918a
TI Expression of branching enzyme II of maize endosperm in Escherichia coli
AU Guan, Han Ping; Baba, Tadashi; Preiss, Jack
CS Department Biochemistry, Michigan State University, East Lansing, MI, 48824, USA
SO Cellular and Molecular Biology (Paris) (1994), 40(7), 981-8
CODEN: CMOBEF; ISSN: 0145-5680
PB C.M.B. Association
DT Journal
LA English
OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)

L8 ANSWER 44 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Genetic isolation, cloning, and analysis of a Mutator-induced, dominant antimorph of the maize amylose extender1 locus
AB The authors report the genetic identification, mol. cloning, and characterization of a dominant mutant at the amylose extender1 locus, Ae1-5180. The identities of the authors' clones are corroborated by their ability to reveal DNA polymorphisms between seven wild-type revertants from Ae1-5180 relative to the Ae1-5180 mutant allele and between four of five independently derived, Mutator (Mu)-induced recessive ae1 alleles relative to their resp. wild-type progenitor alleles. The Ae1-5180 mutation is associated with two Mu1 insertions flanked by complex rearrangements of ae1-related sequences. One of the Mu1 elements is flanked by inverted repeats of ae1-related DNA of at least 5.0 kb in length. This Mu1 element and at least some of this flanking inverted repeat DNA are absent or hypermethylated in six of seven wild-type revertants of Ae1-5180 that were analyzed. The second Mu1 element is flanked on one side by the 5.0-kb ae1-specific repeat and on the other side by a sequence that does not hybridize to the ae1-related repeat sequence. This second Mu1 element is present in revertants to the wild type and does not, therefore, appear to affect ae1 gene function. A 2.7-kb ae1 transcript can be detected in wild-type and homozygous ae1-Ref endosperms 20 days after pollination. This transcript is absent in endosperms containing one, two, or three doses of Ae1-5180. This result is consistent with a suppression model to explain the dominant gene action of Ae1-5180 and establishes Ae1-5180 as an antimorphic allele. Homozygous wild-type seedlings produce no detectable transcript, indicating some degree of tissue specificity for ae1 expression. Sequence analyses establish that ae1 encodes starch branching

enzyme II.
AN 1994:550052 HCAPLUS <<LOGINID::20100610>>
DN 121:150052
OREF 121:26949a,26952a
TI Genetic isolation, cloning, and analysis of a Mutator-induced, dominant antimorph of the maize amylose extender1 locus
AU Stinard, Philip S.; Robertson, Donald S.; Schnable, Patrick S.
CS Dep. Agron., Iowa State Univ., Ames, IA, 50011, USA
SO Plant Cell (1993), 5(11), 1555-66
CODEN: PLCEEW; ISSN: 1040-4651
DT Journal
LA English
OSC.G 62 THERE ARE 62 CAPLUS RECORDS THAT CITE THIS RECORD (62 CITINGS)

L8 ANSWER 45 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Modulating the quantity and quality of starch synthesis in plants by placing the gene for a starch-metabolizing enzyme under control of a regulated promoter
AB A method of producing a plant with switchable starch-synthesizing ability by stably incorporating a target gene for an enzyme involved in a starch or glycogen biosynthetic pathway and under the control of a regulated promoter into the genome of a recipient plant. A plant with controllable starch-synthesizing ability may have switchable starch yield, and/or switchable starch quality. Starch or glycogen biosynthetic enzymes include soluble starch synthase, branching enzyme , glycogen synthase, ADP-glucose pyrophosphorylase, self-glucosylating protein, glycogenin and amylogenin. DNA constructs for use in this method are described, as well as plants transformed with said DNA constructs, the seeds and progeny of such plants, and hybrids whose pedigree includes such plants. The examples demonstrate the functioning of the chemical-inducible promoter of the gene for the 27 kd subunit of glutathione-S-transferase II in maize endosperm and discuss the construction of appropriate expression vectors.
AN 1994:530242 HCAPLUS <<LOGINID::20100610>>
DN 121:130242
OREF 121:23445a,23448a
TI Modulating the quantity and quality of starch synthesis in plants by placing the gene for a starch-metabolizing enzyme under control of a regulated promoter
IN Keeling, Peter Lewis
PA Zeneca Ltd., UK
SO PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9411520	A2	19940526	WO 1993-GB2305	19931109 <--
	WO 9411520	A3	19940804		
	W: AU, BB, BG, BR, BY, CA, CZ, FI, HU, JP, KP, KR, KZ, LK, LV, MG, MN, MW, NO, NZ, PL, RO, RU, SD, SK, UA, US, VN				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9454285	A	19940608	AU 1994-54285	19931109 <--
PRAI	GB 1992-23454	A	19921109	<--	
	WO 1993-GB2305	W	19931109	<--	

OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (22 CITINGS)
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 46 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Expression of branching enzyme I of maize endosperm in Escherichia coli
AB The gene encoding for mature branching enzyme (BE) I (BEI) of maize (Zea mays L.) endosperm has been expressed in Escherichia coli using the T7 promoter. The expressed BEI was purified to near homogeneity so that amylolytic activity and bacterial BE could be completely eliminated from the BE preparation The recombinant enzyme showed properties very similar to those of BEI purified from developing maize endosperm with respect to branching amylose and amylopectin. This result confirmed the authors' earlier report that maize endosperm BEI had a higher rate of branching amylose and a much lower rate (less than 10% of that of branching amylose) of branching amylopectin. This study also showed a great advantage in purifying BE from the bacterial expression system rather than from developing maize endosperm. Most important, this study has established the system with which to study the structure-function relationships of the maize BEI using site-directed mutagenesis.
AN 1994:502618 HCAPLUS <<LOGINID::20100610>>
DN 121:102618
OREF 121:18339a,18342a
TI Expression of branching enzyme I of maize endosperm in Escherichia coli
AU Guan, Han Ping; Baba, Tadashi; Preiss, Jack
CS Dep. Biochem., Michigan State Univ., East Lansing, MI, 48824, USA
SO Plant Physiology (1994), 104(4), 1449-53
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
OSC.G 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)

L8 ANSWER 47 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Differentiation of the properties of the branching isoenzymes from maize (Zea mays)
AB The multiple forms of branching enzyme (BE) from developing maize (Zea mays) endosperm were purified by modification of previous procedures such that amylase activity could be eliminated completely from the BE preparation Three distinct assays for BE activity (phosphorylase a stimulation assay, BE linkage assay, and iodine stain assay) were used to characterize and differentiate the properties of the BE isoforms. This study presents the first evidence that the BE isoforms differ in their action on amylopectin. BEI had the highest activity in branching amylose, but its rate of branching amylopectin was less than 5% of that of branching amylose. Conversely, BEII isoforms had lower rates in branching amylose (about 9-12% of that of BEI) and had higher rates of branching amylopectin (about 6-fold) than BEI. The implication of these findings to the mechanism of amylopectin synthesis in vivo are discussed.
AN 1994:48576 HCAPLUS <<LOGINID::20100610>>
DN 120:48576
OREF 120:8791a,8794a
TI Differentiation of the properties of the branching isoenzymes from maize (Zea mays)
AU Guan, Han Ping; Preiss, Jack
CS Dep. Biochem., Michigan State Univ., East Lansing, MI, 48824, USA
SO Plant Physiology (1993), 102(4), 1269-73
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
OSC.G 113 THERE ARE 113 CAPLUS RECORDS THAT CITE THIS RECORD (113 CITINGS)

L8 ANSWER 48 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Starch branching enzyme II from
maize endosperm
AB The authors report here the cloning of a SBE II cDNA from maize.
Three λgt10 cDNA libraries were constructed from endosperm poly(A)+
RNA 14, 22, and 29 DAP. A heterologous nucleic acid probe, clone pJSBE5,
the cDNA for pea SBE I, was used to screen the 14-DAP library. After
purifying and subcloning into plasmid pBluescript II SK- (Stratagene), a
full-length cDNA of 2725 bp was isolated. Northern blots of total
maize RNA isolated from endosperm tissue 12 DAP and probed with
the cloned maize cDNA revealed a single transcript of approx.
2.7 kb. Deduced amino acid sequence was compared with the pea SBE I
(Bhattacharya et al., 1990), maize SBE I (Baba et al., 1991),
and rice SBE I (Nakamura et al., 1992) translated cDNA sequences using
Intelligenetics software. Levels of residue identify were 71, 52, and
52%, resp. From these results, the authors conclude that they have cloned
a second isoform of SBE from maize endosperm. This conclusion
is supported by the N-terminal sequence of purified maize SBE
IIb protein, which matches the cDNA predicted amino acid sequence at
residues 58 to 65. The addnl. amino acid residues making up the
N-terminal end of the deduced sequence are thought to encode a transit
peptide (53 amino acids) for routing of the protein to the amyloplast.
The deduced mol. weight of the mature protein from this sequence data is
84,772. This is slightly larger than size ests. of 80,000 D based upon
SDS-PAGE anal. of purified SBE IIa and IIb protein (Boyer and Preiss,
1978; Singh and Preiss, 1985).
AN 1993:621872 HCAPLUS <<LOGINID::20100610>>
DN 119:221872
OREF 119:39477a,39480a
TI Starch branching enzyme II from
maize endosperm
AU Fisher, Dane K.; Boyer, Charles D.; Hannah, L. Curtis
CS Dep. Hortic., Pennsylvania State Univ., University Park, PA, 16802, USA
SO Plant Physiology (1993), 102(3), 1045-6
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
OSC.G 63 THERE ARE 63 CAPLUS RECORDS THAT CITE THIS RECORD (64 CITINGS)

L8 ANSWER 49 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Starch branching enzyme cDNA from Solanum
tuberosum
AB A full-length cDNA clone encoding starch branching
enzyme (SBE, E.C. 2.4.1.18) was isolated from a Solanum tuberosum
sprout cDNA library using a partial potato SBE cDNA clone that was
originally isolated with a heterologous cDNA encoding a pea SBE. The 3114
bp DNA sequence revealed an ORF which encodes an 861 amino acid protein
which has significant similarity to SBE I from maize and rice.
The protein has a calculated Mr of 99,083. The SBE amino terminus has some
features in common with chloroplast transit peptides, i.e. a high content
of Ser and Thr residues and a central, pos. charged domain. Also, the
hydropathicity profiles of the amyloplast transit peptide from the potato
granule-bound starch synthase and the amino terminus of SBE are similar.
AN 1993:554604 HCAPLUS <<LOGINID::20100610>>
DN 119:154604
OREF 119:27569a,27572a
TI Starch branching enzyme cDNA from Solanum
tuberosum
AU Poulsen, Peter; Kreiberg, Jette D.
CS MARIBO Seed, Biotechnol., Copenhagen, DK-1001, Den.
SO Plant Physiology (1993), 102(3), 1053-4
CODEN: PLPHAY; ISSN: 0032-0889

DT Journal
LA English
OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)

L8 ANSWER 50 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Starch branching enzymes from immature rice seeds
AB Four forms of branching enzyme, termed RBE1, RBE2 (a mixture of RBE2A and RBE2B), RBE3, and RBE4, were apparently separated by DEAE-cellulose column chromatog. of soluble extract from immature rice seeds, and each of these 4 forms was further purified by gel-filtration. RBE1, RBE2A, and RBE2B were the predominant forms of the enzyme. The mol. size, N-terminal amino acid sequence, and immunoreactivity with anti-maize branching enzyme-I (BE-I) antibody were identical among these 3 forms, except that the mol. mass of RBE2A was almost 3 kDa higher than those of RBE1 and RBE2B. These results indicate that RBE1, RBE2A, and RBE2B are the same; the enzyme is termed rice BE-I. The cDNA clones coding for rice BE-1 were identified from a rice seed library in γgt11, using the maize BE-I cDNA as a probe. The nucleotide sequence indicates that rice BE-I is initially synthesized as an 820-residue precursor protein, including a putative 64- or 66-residue transit peptide at the N terminus. The rice mature BE-I contains 756 (or 754) amino acids with a calculated mol. mass of 86,734 (or 86,502) Da, and shares a high degree of sequence identity (86%) with the maize protein. The consensus sequences of the 4 regions that form the catalytic sites of amylolytic enzymes are conserved in the central region of the rice BE-I sequence. Thus, rice BE-I as well as the maize protein belongs to a family of amylolytic enzymes.
AN 1993:512080 HCAPLUS <<LOGINID::20100610>>
DN 119:112080
OREF 119:20053a,20056a
TI Starch branching enzymes from immature rice seeds
AU Mizuno, Kouichi; Kimura, Koji; Arai, Yuji; Kawasaki, Tsutomu; Shimada, Hiroaki; Baba, Tadashi
CS Inst. Appl. Biochem., Univ. Tsukuba, Tsukuba, 305, Japan
SO Journal of Biochemistry (1992), 112(5), 643-51
CODEN: JOBIAO; ISSN: 0021-924X
DT Journal
LA English
OSC.G 46 THERE ARE 46 CAPLUS RECORDS THAT CITE THIS RECORD (46 CITINGS)

L8 ANSWER 51 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Branching of amylose by the branching isoenzymes of maize endosperm
AB A convenient, quant. assay method of branching enzyme (BE) was devised with reduced amylose as the substrate. Using this assay, the properties of the purified branching isoenzymes from maize, BE I, IIa, and IIb, were studied. The method is based on determination of reducing power, by the modified Park-Johnson method, of the chains transferred by BE after they are released from the branched products with isoamylase. The optimum pH of the three enzymes is 7.5, and the optimum temps. of BE I, IIa, and IIb are 33, 25, and 15-20°, resp. The specific activities are highest for BE I and the lowest for BE IIb, whereas in the conventional assay based on stimulation of unprimed phosphorylase activity, the specific activities are BE IIb > IIa > I. BE I has a lower Km (2.0 μM of the nonreducing terminal) for the reduced amylose of average chain-length (.hivin.cl) 405 than BE IIa (10 μM) and the IIb (11 μM), and the enzyme shows a higher Km for reduced amyloses of smaller .hivin.cl. Gel-permeation chromatograms on Sephadex G-75SF of the chain transferred from the reduced amylose indicate that initially the three isoenzymes produced chains of various sizes (d.p. .apprx.8 to >200), and BE I

preferentially transfers longer chains than BE IIa and IIb.
AN 1993:186425 HCAPLUS <<LOGINID::20100610>>
DN 118:186425
OREF 118:31875a,31878a
TI Branching of amylose by the branching isoenzymes of maize endosperm
AU Takeda, Yasuhito; Guan, Han Ping; Preiss, Jack
CS Dep. Biochem., Michigan State Univ., East Lansing, MI, 48824, USA
SO Carbohydrate Research (1993), 240, 253-63
CODEN: CRBRAT; ISSN: 0008-6215
DT Journal
LA English
OSC.G 104 THERE ARE 104 CAPLUS RECORDS THAT CITE THIS RECORD (104 CITINGS)

L8 ANSWER 52 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Characterization of the (1 → 4)-α-D-glucan-branching 6-glycosyltransferase by in vitro synthesis of branched starch polysaccharides
AB Starch branching enzyme (Q-enzyme; EC 2.4.1.18) (I), isolated from young, mature potato tubers and purified by (NH4)2SO4 precipitation, hydrophobic chromatog., and size-exclusion chromatog., was found to be completely free of phosphorylase (EC 2.4.1.1) and α-amylase (EC 3.2.1.1) activities. I had a mol. weight of 64 kDa, was homogeneous in SDS-PAGE, was inhibited by 4 + 10-5 M oxidized glutathione, and could be stored at -80° in the presence of SH group-reducing agents. The actions of I alone, and in combination with potato phosphorylase, on amylose, pea starch, potato amylose, potato amylopectin, and waxy maize was investigated. The combination gave high-mol.-weight polysaccharides, debranching of which yielded patterns of short and long chains similar to those of debranched amylopectin. Treatment of amylose with I resulted in a decrease in the average mol. weight and
in the broadening of the mol. weight distribution; debranching of the product yielded a short-chain distribution pattern.
AN 1992:250852 HCAPLUS <<LOGINID::20100610>>
DN 116:250852
OREF 116:42415a,42418a
TI Characterization of the (1 → 4)-α-D-glucan-branching 6-glycosyltransferase by in vitro synthesis of branched starch polysaccharides
AU Praznik, Werner; Rammesmayer, Gerald; Spies, Thomas
CS Inst. Chem., Univ. Bodenkul., Vienna, A-1180, Austria
SO Carbohydrate Research (1992), 227, 171-82
CODEN: CRBRAT; ISSN: 0008-6215
DT Journal
LA English
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L8 ANSWER 53 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Comparison of soluble starch synthases and branching enzymes from leaves and kernels of normal and amylose-extender maize
AB Soluble starch synthases (SS) and branching enzymes (BE) from 20-day-old maize leaves and 22-day-old seeds of normal and amylose-extender (ae) were purified by DEAE-cellulose chromatog. Elution profiles of leaf exts. showed 1 major SS and 2 BE fractions from both genotypes. The SS fractions from normal and ae leaf exts. were capable of citrate-stimulated starch synthesis and had different reaction rates with various primers. The 2 BE fractions from normal leaf exts. differed significantly from each other but not when compared to the same BE from ae. Comparison of BE fractions from ae and normal leaves showed no differences based on chromatog., kinetic, and immunol. properties. Comparison of the leaf

enzymes with endosperm enzymes showed major differences. Leaf exts. did not contain SSII or BEIIb observed in endosperm exts. Developing ae endosperm lacked BEIIb activity and ae was the structural gene for BEIIb. The tissue-specific expression of BEIIb in the endosperm provided the basis for explaining the tissue-specific expression of ae. It was proposed that as BEIIb is expressed in the endosperm, but not leaves, allelic substitution at the ae locus modifies only endosperm starch synthesis.

AN 1990:94355 HCAPLUS <<LOGINID::20100610>>
DN 112:94355
OREF 112:15955a,15958a
TI Comparison of soluble starch synthases and branching enzymes from leaves and kernels of normal and amylose-extender maize
AU Dang, Peter L.; Boyer, Charles D.
CS Dep. Hort., Pennsylvania State Univ., University Park, PA, 16802, USA
SO Biochemical Genetics (1989), 27(9-10), 521-32
CODEN: BIGEBA; ISSN: 0006-2928
DT Journal
LA English
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L8 ANSWER 54 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI The wrinkled-seed character of pea described by Mendel is caused by a transposon-like insertion in a gene encoding starch-branching enzyme
AB The r (rugosus) locus of pea (Pisum sativum L.), which dets. whether the seed is round or wrinkled, was cloned. Wrinkled (rr) seeds lack one isoform of starch-branching enzyme (SBEI), present in round (RR or Rr) seeds. A major polymorphism in the SBEI gene between near-isogenic RR and rr lines shows 100% cosegregation with the r locus, establishing that the SBEI gene is at the r locus. An aberrant transcript for SBEI is produced in rr embryos. In rr lines, the SBEI gene is interrupted by an 0.8 kb insertion that is very similar to the Ac/Ds family of transposable elements from maize. Failure to produce SBEI has complex metabolic consequences on starch, lipid, and protein biosynthesis in the seed.
AN 1990:93044 HCAPLUS <<LOGINID::20100610>>
DN 112:93044
OREF 112:15703a,15706a
TI The wrinkled-seed character of pea described by Mendel is caused by a transposon-like insertion in a gene encoding starch-branching enzyme
AU Bhattacharyya, Madan K.; Smith, Alison M.; Ellis, T. H. Noel; Hedley, Cliff; Martin, Cathie
CS John Innes Inst., AFRC Inst. Plant Sci. Res., Norwich, NR4 7UH, UK
SO Cell (Cambridge, MA, United States) (1990), 60(1), 115-22
CODEN: CELLB5; ISSN: 0092-8674
DT Journal
LA English
OSC.G 110 THERE ARE 110 CAPLUS RECORDS THAT CITE THIS RECORD (110 CITINGS)

L8 ANSWER 55 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Immunological comparison of the starch branching enzymes from potato tubers and maize kernels
AB Starch branching enzyme was purified from potato (Solanum tuberosum) tubers as a single species of 79 kilodaltons and specific antibodies were prepared against both the native enzyme and against the gel-purified, denatured enzyme. The activity of potato branching enzyme could only be neutralized by antinative potato branching enzyme, whereas both types of antibodies reacted with denatured potato branching enzyme. Starch branching enzymes were also isolated from

maize (Zea mays) kernels. All of the denatured forms of the maize enzyme reacted with antidenatured potato branching enzyme, whereas recognition by antinative potato branching enzyme was limited to maize branching enzymes I and IIb. Antibodies directed against the denatured potato enzyme were unable to neutralize the activity of any of the maize branching enzymes. Antinative potato branching enzyme fully inhibited the activity of maize branching enzyme I; the neutralized maize enzyme was identified as a 82 kilodalton protein. Thus, potato branching enzyme (Mr = 79,000) shares a high degree of similarity with maize branching enzyme I (Mr = 82,000), in the native as well as the denatured form. Cross-reactivity between potato branching enzyme and the other forms of maize branching enzyme was observed only after denaturation, which suggests mutual sequence similarities between these species.

AN 1989:454197 HCAPLUS <<LOGINID::20100610>>
DN 111:54197
OREF 111:9149a,9152a
TI Immunological comparison of the starch branching enzymes from potato tubers and maize kernels
AU Vos-Scheperkeuter, Greetje H.; De Wit, Janny G.; Ponstein, Anne S.; Feenstra, Will J.; Witholt, Bernard
CS Dep. Biochem., Groningen Biotechnol. Cent., Groningen, 9747 AG, Neth.
SO Plant Physiology (1989), 90(1), 75-84
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)

L8 ANSWER 56 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Maize leaf and kernel starch synthases and starch branching enzymes
AB Soluble starch synthases and branching enzymes were partially purified from developing leaves and kernels of maize using DEAE-cellulose chromatog. One form of starch synthase and 2 forms of branching enzyme were detected in leaves as compared to 2 forms of starch synthase and 3 forms of branching enzyme isolated from the kernels. The starch synthase fraction from the leaves and the 1st starch synthase fraction from the kernels showed greater activity in reactions containing various glycogens as primers than in those containing amylopectin. In addition, both were capable of synthesizing a polyglucan in the absence of an added primer but in the presence of Na citrate and bovine serum albumin (citrate-stimulated starch synthesis). The 2nd starch synthase fraction from kernels showed greater activity with amylopectin as primer and had no citrate-stimulated activity. The leaf enzyme and endosperm starch synthase I are suggested to be the same enzyme and constitutively expressed. Branching enzymes from leaves and kernels differed not only in their elution profiles but also their stimulation of phosphorylase a (assay A) and amylose branching (assay B) activities. A minor branching enzyme fraction from leaves (leaf branching enzyme I) eluted from the DEAE-cellulose column after the addition of a salt gradient, whereas branching enzyme I from kernels eluted in the buffer wash prior to the application of the gradient. However, the ratios of assay A to assay B suggested that branching enzyme I from leaves was catalytically similar to branching enzyme I from the kernels. The major leaf branching enzyme (branching enzyme II) eluted at the same position from the DEAE-cellulose column as endosperm branching enzyme IIa. These enzymes had similar ratios of activity (assay A/assay B). The cross-reaction of leaf branching enzymes with antisera prepared against maize endosperm branching enzymes in immunodiffusion expts. and enzyme activity neutralization expts. further demonstrated the relationship of the leaf and endosperm branching enzymes.

AN 1988:434288 HCAPLUS <<LOGINID::20100610>>
DN 109:34288
OREF 109:5733a,5736a
TI Maize leaf and kernel starch synthases and starch branching enzymes
AU Dang, Peter L.; Boyer, Charles D.
CS Dep. Hortic., Pennsylvania State Univ., University Park, PA, 16802, USA
SO Phytochemistry (1988), 27(5), 1255-9
CODEN: PYTCAS; ISSN: 0031-9422
DT Journal
LA English
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)

L8 ANSWER 57 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Enzyme activities associated with maize kernel amyloplasts
AB Activities of the enzymes of gluconeogenesis and of starch metabolism were measured in exts. of amyloplasts isolated from protoplasts derived from 14-day olid maize (Zea mays cv Pioneer 3780) endosperm. The enzymes triosephosphate isomerase, fructose-1,6-bisphosphate aldolase, fructose-1,6-bisphosphatase, phosphohexose isomerase, phosphoglucomutase, ADPG pyrophosphorylase, UDPG pyrophosphorylase, soluble and bound starch synthases, and branching enzyme were present in the amyloplasts. Of the above enzymes, ADPG pyrophosphorylase had the lowest activity per amyloplast. Invertase, sucrose synthase, and hexokinase were not detected in similar amyloplast prepns. Only a trace of the cytoplasmic marker enzyme alc. dehydrogenase could be detected in purified amyloplast fractions. Also, purified amyloplasts were lysed and then supplied with radioactive glucose-6-phosphate, glucose-1-phosphate, fructose-1,6-bisphosphate, dihydroxyacetone phosphate, glucose, fructose, sucrose, and 3-O-methylglucose in the presence of ATP or uridine triphosphate. Of the above, only the phosphorylated substrates were incorporated into starch. Incorporation into starch was higher with added uridine triphosphate than with ATP. Dihydroxyacetone phosphate was the preferred substrate for uptake by intact amyloplasts and incorporation into starch. In preliminary expts., it appeared that glucose-6-P and fructose-1,6-bisphosphate may also be taken up by intact amyloplasts. However, the rate of uptake and incorporation into starch was relatively low and variable. Addnl. study is needed to determine conclusively whether hexose phosphates will cross intact amyloplast membranes. Thus: (a) triose phosphate is the preferred substrate for uptake by intact amyloplasts; (b) amyloplasts contain all enzymes necessary to convert triose phosphates into starch; (c) sucrose breakdown must occur in the cytosol prior to carbohydrate transfer into the amyloplasts; (d) under the conditions of assay, amyloplasts are unable to convert glucose or fructose to starch; (e) uridine triphosphate may be the preferred nucleotide for conversion of hexose phosphates to starch at this stage of kernel development.
AN 1988:201823 HCAPLUS <<LOGINID::20100610>>
DN 108:201823
OREF 108:33085a,33088a
TI Enzyme activities associated with maize kernel amyloplasts
AU Echeverria, Edgardo; Boyer, Charles D.; Thomas, Paul A.; Liu, Kang Chien; Shannon, Jack C.
CS Dep. Hortic., Pennsylvania State Univ., University Park, PA, 16802, USA
SO Plant Physiology (1988), 86(3), 786-92
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)

L8 ANSWER 58 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Biosynthesis of starch; identification of potato starch enzymes
AB Two important starch enzymes, granule-bound starch synthase and branching enzyme, were purified from potato tubers and characterized by immunol. comparison with the corresponding enzymes of other plants. Granule-bound starch synthase was identified as a 60-kilodalton (kd) protein homologous to the corresponding enzymes of maize and amaranth; the enzyme was missing in amylose-free potato starch granules. Branching enzyme of potato tubers was purified as a single protein species of 79 kd which appeared to be homologous to maize branching enzyme I, but much less to branching enzymes IIa and IIb.
AN 1988:127390 HCAPLUS <<LOGINID::20100610>>
DN 108:127390
OREF 108:20801a,20804a
TI Biosynthesis of starch; identification of potato starch enzymes
AU Vos-Scheperkeuter, G. H.; Ponstein, A. S.; De Wit, J. G.; Feenstra, W. J.; Oostergetel, G. T.; Van Bruggen, E. F. J.; Witholt, B.
CS Dep. Biochem., Groningen Biotechnol. Cent., Groningen, 9747 AG, Neth.
SO Food Hydrocolloids (1987), 1(5-6), 387-91
CODEN: FOHYES; ISSN: 0268-005X
DT Journal
LA English

L8 ANSWER 59 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Regulation of starch synthesis in Zea mays leaves
AB The kinetic properties of bundle sheath and mesophyll-specific ADP-glucose pyrophosphorylases (I) were studied with respect to the known localization of starch biosynthesis in the bundle sheath cells of maize. At least 75% of starch synthase and branching enzyme and 95% of I were in the bundle sheath; starch-degrading enzymes were more evenly distributed between cell types. Partially purified I from the 2 cell types were characterized by pH optima, substrate affinities, and regulatory properties. The bundle sheath enzyme was activated by 3-phosphoglycerate and other organic phosphates to a greater extent than was the mesophyll enzyme, and the bundle sheath enzyme was also less sensitive to phosphate inhibition. Thus, in vivo activity of maize leaf I as well as starch synthesis may be controlled by the levels of the enzymes in specific cell types and by the allosteric properties of I.
AN 1987:493580 HCAPLUS <<LOGINID::20100610>>
DN 107:93580
OREF 107:15227a,15230a
TI Regulation of starch synthesis in Zea mays leaves
AU Spilatro, Steven R.; Preiss, Jack
CS Dep. Biochem., Michigan State Univ., East Lansing, MI, 48824, USA
SO Prog. Photosynth. Res., Proc. Int. Congr. Photosynth., 7th (1987), Meeting Date 1986, Volume 3, 701-4. Editor(s): Biggins, John. Publisher: Nijhoff, Dordrecht, Neth.
CODEN: 55RQAT
DT Conference
LA English

L8 ANSWER 60 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Localization of starch biosynthetic and degradative enzymes in maize leaves
AB The cellular distribution of the starch biosynthetic and degradative enzymes in protoplasts prepared from maize (Zea mays) leaf mesophyll and bundle sheath cells was investigated. In conformity with the cellular distribution of starch, starch biosynthetic enzymes (soluble starch synthase, ADP glucose pyrophosphorylase, branching enzyme, and starch phosphorylase) were exclusively

localized in the bundle sheath cells. In contrast, starch degradative enzymes (α-amylase, β-amylase, and debranching enzyme) were present in both types of leaf cells. Isolated chloroplasts from bundle sheath cells contained 100% of the starch biosynthetic enzymes. However, .apprx.60% of the activity of degradative enzymes and 67% of the activity of starch phosphorylase was localized in bundle sheath chloroplasts.
AN 1986:222052 HCAPLUS <<LOGINID::20100610>>
DN 104:222052
OREF 104:35153a,35156a
TI Localization of starch biosynthetic and degradative enzymes in maize leaves
AU Echeverria, Edgardo; Boyer, Charles D.
CS Dep. Hortic., Pennsylvania State Univ., University Park, PA, 16802, USA
SO American Journal of Botany (1986), 73(2), 167-71
CODEN: AJBOAA; ISSN: 0002-9122
DT Journal
LA English
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)

L8 ANSWER 61 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Starch branching enzymes from maize. Immunological characterization using polyclonal and monoclonal antibodies
AB Spleen cells from mice immunized with starch-branching enzymes were fused with cells from the mouse myeloma Sp2/0-AG14 cell line to form hybridomas. Those hybridomas producing antibodies against the branching enzyme were screened by the ELISA using purified branching enzyme as the antigen. Three monoclonal cell lines (1A1D7, 1A1C3, and 4D2A9D8) were found to produce antibodies which showed pos. ELISA reactions with maize branching enzyme I in addition to branching enzymes IIa and IIb. Three other monoclonal cell lines (4D2D10, 4D2F9, and 2A6C12) were also selected which produced antibodies showing pos. ELISA reactions with branching enzymes IIa and IIb only. The amino acid composition and peptide maps obtained after trypsin or chymotrypsin digestion show that there is no difference between branching enzymes IIa and IIb, but they are significantly different from branching enzyme I, which, along with immunol. data, suggests that only 2 forms of starch-branching enzyme may be present in maize kernels. Immunol. cross-reaction was also found between the starch-branching enzyme from maize kernels and the glycogen-branching enzyme from Escherichia coli, using polyclonal antibodies against starch-branching enzyme I or IIa and IIb or E. coli glycogen-branching enzyme, suggesting some immunol. similarities between maize starch-branching enzymes and E. coli glycogen-branching enzyme.
AN 1985:591998 HCAPLUS <<LOGINID::20100610>>
DN 103:191998
OREF 103:30836h,30837a
TI Starch branching enzymes from maize. Immunological characterization using polyclonal and monoclonal antibodies
AU Singh, Bijay K.; Preiss, Jack
CS Dep. Biochem. Biophys., Univ. California, Davis, CA, 95616, USA
SO Plant Physiology (1985), 79(1), 34-40
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)

L8 ANSWER 62 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Immunological characterization of maize starch branching enzymes
AB Highly purified fractions of 3 starch-branching enzymes from developing maize endosperm were used to prepare antisera in rabbits. In double

diffusion expts., no immunoppt. was observed when branching enzyme IIa or IIb was tested against branching enzyme I antiserum. No immunoppt. was formed when branching enzyme I was tested against branching enzyme IIa or IIb antiserum. Increasing amts. of antisera in the above combinations also failed to inhibit enzyme activity. Branching enzyme IIa antiserum cross-reacted and formed spurs with branching enzyme IIb when compared with branching enzyme IIa antigen. Comparison of branching enzyme IIb antiserum with branching enzyme IIa also resulted in an immunoppt. Increasing levels of branching enzyme IIa antiserum inhibited branching enzyme IIb as did the reciprocal combination. Thus, branching enzymes IIa and IIb are immunol. similar, whereas branching enzyme I is distinct. The data supports the classification of starch-branching enzymes based on genetic, kinetic, and chromatog. properties.

AN 1983:484351 HCAPLUS <<LOGINID::20100610>>
DN 99:84351
OREF 99:12965a,12968a
TI Immunological characterization of maize starch branching enzymes
AU Fisher, Mary B.; Boyer, Charles D.
CS Dep. Hortic., Pennsylvania State Univ., University Park, PA, 16802, USA
SO Plant Physiology (1983), 72(3), 813-16
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

L8 ANSWER 63 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Gene dosage at the amylose-extender locus of maize: effects on the levels of starch branching enzymes
AB Soluble starch-branching enzymes and starch synthases from corn kernels of differing dosage of the ae locus were purified by DEAE-cellulose chromatog. A near-linear relation between increasing dosage of the dominate amylose-extender allele (Ae) and branching enzyme IIb activity was found. In contrast, levels and properties of branching enzymes I and IIa, as well as the citrate-stimulated and primer-requiring starch synthases, remained unchanged. The near-linear increase in branching enzyme IIb activity with increasing doses of the Ae allele is consistent with the hypothesis that ae is the structural gene coding for branching enzyme IIb.

AN 1982:488902 HCAPLUS <<LOGINID::20100610>>
DN 97:88902
OREF 97:14769a,14772a
TI Gene dosage at the amylose-extender locus of maize: effects on the levels of starch branching enzymes
AU Hedman, Karen D.; Boyer, Charles D.
CS Dep. Hortic. For., Rutgers, State Univ., New Brunswick, NJ, 08903, USA
SO Biochemical Genetics (1982), 20(5-6), 483-92
CODEN: BIGEBA; ISSN: 0006-2928
DT Journal
LA English
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)

L8 ANSWER 64 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Evidence for independent genetic control of the multiple forms of maize endosperm branching enzymes and starch synthases
AB Soluble starch synthase and starch-branching enzymes in exts. from kernels of 4 corn genotypes were compared. Exts. from normal (nonmutant) corn were found to contain 2 starch synthases and 3 branching enzyme fractions. The different fractions could be distinguished by chromatog. properties and kinetic properties under various assay conditions. Kernels homozygous for the recessive amylose-extender (ae) allele were missing branching enzyme IIb. In addition, the

citrate-stimulated activity of starch synthase I was reduced. This activity could be regenerated by the addition of branching enzyme to this fraction. No other starch synthase fractions were different from normal enzymes. Exts. from kernels homozygous for the recessive dull (du) allele were found to contain lower branching enzyme IIa and starch synthase II activities. Other fractions were not different from the normal enzymes. Anal. of exts. from kernels of the double mutant ae du indicated that the 2 mutants act independently. Branching enzyme IIb was absent and the citrate-stimulated reaction of starch synthase I was reduced but could be regenerated by the addition of branching enzyme (ae properties) and both branching enzyme IIa and starch synthase II were greatly reduced (du properties). Starch from ae and du endosperms contains higher amylose (66 and 42%, resp.) than normal endosperm (26%). In addition, the amylopectin fraction of ae starch is less highly branched than amylopectin from normal or du starch. The above observations suggest that the alterations of the starch may be accounted for by changes in the soluble synthase and branching enzyme fractions.

AN 1981:458224 HCAPLUS <<LOGINID::20100610>>
DN 95:58224
OREF 95:9805a,9808a
TI Evidence for independent genetic control of the multiple forms of maize endosperm branching enzymes and starch synthases
AU Boyer, Charles D.; Preiss, Jack
CS Dep. Biochem. Biophys., Univ. California, Davis, CA, 95616, USA
SO Plant Physiology (1981), 67(6), 1141-5
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
OSC.G 56 THERE ARE 56 CAPLUS RECORDS THAT CITE THIS RECORD (56 CITINGS)

L8 ANSWER 65 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Evidence for independent genetic control of the multiple forms of maize endosperm branching enzymes and starch synthases
AB Two forms of starch synthase (EC 2.4.1.21) were isolated from an (NH4)2SO4 fraction of dent maize endosperm extract by DEAE-cellulose chromatog. Synthase I had higher activity with glycogen than amylopectin as a primer, whereas synthase II had higher activity with amylopectin. Both enzyme had a Km for ADP-glucose of 0.10 mM. Three forms of branching enzyme (EC 2.4.1.18) were also separated from maize endosperm on DEAE-cellulose. Fraction I was observed in the void volume, whereas fractions IIa and IIb coeluted with starch synthase I and II, resp. These enzymes were examined in 2 maize mutants with altered starch structure. Starch from amylose-extender (ae) mutant endosperm contained a higher proportion of linear amylose and amylopectin with fewer branch points than normal amylopectin. Normal starch synthase I and II levels were observed in ae mutants, but most if not all branching enzyme activity associated with starch synthase I was missing. The dull mutant, which also contains a higher than normal proportion of amylose, contained normal levels of starch synthase I and branching enzyme I but a significant (60%) decrease in starch synthase II activity and a small decrease in branching enzyme activity associated with starch synthase II fractions was observed
AN 1981:420241 HCAPLUS <<LOGINID::20100610>>
DN 95:20241
OREF 95:3500h,3501a
TI Evidence for independent genetic control of the multiple forms of maize endosperm branching enzymes and starch synthases
AU Preiss, Jack; Boyer, Charles D.
CS Dep. Biochem. Biophys., Univ. California, Davis, CA, USA

SO Mech. Saccharide Polym. Depolym., [Proc. Symp.] (1980), Meeting Date 1978, 161-74. Editor(s): Marshall, James John. Publisher: Academic, New York, N. Y.
CODEN: 45MHAY
DT Conference
LA English
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

L8 ANSWER 66 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI The citrate-stimulated starch synthase of starchy maize kernels: purification and properties
AB Chromatog. of the maize kernel exts. on DEAE-cellulose resolves 2 fractions of starch synthase activity, on of which (starch synthase I) is capable of synthesizing α-glucan in the absence of exogenous primer and the presence of 0.5M citrate (J. L. Ozbun, et al., 1971). This starch synthase was purified 200-fold from developing kernels of normal maize, and shown to have no detectable activities of branching enzyme, amylase, pullulanase, phosphorylase, or D enzyme. The preparation, however, was not electrophoretically homogeneous. This preparation had a Km of 0.033 mM for ADP/glucose in the presence of 0.05M citrate. The reaction in the presence of citrate was stimulated 10-fold by the addition of excess purified branching enzyme. This stimulation is higher than those reported previously, but is consistent with the predicted effects of removal of amylase activity. The effects of salts other than citrate on activity in the absence of exogenous primer were small, but the stimulation could be restored by the addition of excess purified branching enzyme. Citrate increased the affinity of the enzyme for the endogenous primer present to such a level that no effect of exogenous primer on reaction rate could be observed in the presence of 0.5M citrate. Anal. of the glucan-iodine complex and the enzymic breakdown products patterns from the products of the starch synthase reaction indicates a high degree of linearity. The results obtained are discussed in relation to the biosynthesis of starch in vivo.
AN 1980:599890 HCAPLUS <<LOGINID::20100610>>
DN 93:199890
OREF 93:31814h,31815a
TI The citrate-stimulated starch synthase of starchy maize kernels: purification and properties
AU Pollock, Christopher; Preiss, Jack
CS Dep. Biochem. Biophys., Univ. California, Davis, CA, 95616, USA
SO Archives of Biochemistry and Biophysics (1980), 204(2), 578-88
CODEN: ABBIA4; ISSN: 0003-9861
DT Journal
LA English
OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)

L8 ANSWER 67 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Properties of citrate-stimulated starch synthesis catalyzed by starch synthase I of developing maize kernels
AB Starch synthase I, purified .apprx.1000-fold from corn kernels homozygous for the endosperm mutant amylose-extender (ae), was capable of synthesis in the absence of added primer and in the presence of 0.5 M citrate. Because ae endosperm lacks the starch-branching enzyme which normally purifies with starch synthase I, the final enzyme fraction derived was free of detectable branching activity, permitting a detailed characterization of the citrate-stimulated reaction. This reaction was dependent on citrate concns. of >0.1 M. The reaction was not specific for citrate, however, since malate also stimulated the reaction. Branching enzyme increased the velocity of the reaction .apprx.4-fold, but did not replace the requirement for citrate. The Km values for the primers amylopectin and glycogen were lowered by

citrate from 122 and 595 to 6 and 50 μg/mL, resp. The enzyme contained 1.7 mg of anhydroglucose units/enzyme unit. Thus, reaction mixts. contained 1-5 μg (5-25 μg/mL) of endogenous primer. The citrate-stimulated reaction may be explained as an increased affinity for this endogenous primer. The starch synthase reaction in the absence of primer was dependent on several factors, including endogenous primer concentration, citrate concentration, and branching enzyme concentration

AN 1980:72789 HCAPLUS <<LOGINID::20100610>>
DN 92:72789
OREF 92:11953a,11956a
TI Properties of citrate-stimulated starch synthesis catalyzed by starch synthase I of developing maize kernels
AU Boyer, Charles D.; Preiss, Jack
CS Dep. Biochem. Biophys., Univ. California, Davis, CA, 95616, USA
SO Plant Physiology (1979), 64(6), 1039-42
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)

L8 ANSWER 68 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Multiple forms of (1 → 4)-α-D-glucan, (1 → 4)-α-D-glucan-6-glycosyl transferase from developing Zea mays L. kernels
AB Two major forms of branching enzyme from developing kernels of maize were detected by DEAE-cellulose chromatog. Branching-enzyme I eluted with the column wash and was unassocd. with starch-synthase activity. Branching-enzyme II was bound to DEAE-cellulose and was coeluted with both primed and unprimed starch-synthase activities. Both fractions were further purified by chromatog. on aminoalkyl-Sepharose columns. Native and subunit mol. wts. were estimated at 70,000-90,000 for both enzymes. Thus both enzymes are primarily monomeric. Branching-enzymes I and II could be distinguished by chromatog. on DEAE-cellulose or 4-aminobutyl-Sepharose, and by disk-gel electrophoresis with activity staining. Branching-enzyme I had a lower ratio of activity (phosphorylase stimulation-amylose branching). The ratio varied from 30-60 as compared to .apprx.300-500 for branching-enzyme II. Likewise, branching-enzyme I had a lower Km value for amylose than branching-enzyme II. Both enzymes could introduce further branches into amylopectin. Combined action of the branching enzymes and rabbit-muscle phosphorylase a resulted in similar patterns of incorporation of D-glucose into the growing α-D-glucan and the synthesis of high-mol-weight polymers. However, the α-D-glucans differed, as shown by spectra of I complexes and average unit-chain length. Branching-enzyme II was separated into 2 fractions (IIa and IIb) by chromatog. on 4-aminobutyl-Sepharose.
AN 1978:165893 HCAPLUS <<LOGINID::20100610>>
DN 88:165893
OREF 88:26105a,26108a
TI Multiple forms of (1 → 4)-α-D-glucan, (1 → 4)-α-D-glucan-6-glycosyl transferase from developing Zea mays L. kernels
AU Boyer, Charles D.; Preiss, Jack
CS Dep. Biochem. Biophys., Univ. California, Davis, CA, USA
SO Carbohydrate Research (1978), 61(1), 321-34
CODEN: CRBRAT; ISSN: 0008-6215
DT Journal
LA English
OSC.G 76 THERE ARE 76 CAPLUS RECORDS THAT CITE THIS RECORD (76 CITINGS)

L8 ANSWER 69 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Multiple forms of starch branching enzyme of maize: evidence for independent genetic control

AB Purification of starch-branching enzymes from kernels of 2 nonlinked mutants of maize, sugary and amylose-extender, showed the basis of the 2 mutations to be associated with the previously identified branching enzymes I and IIb, resp. Branching enzyme I from sugary kernels was purified the same as nonmutant branching enzyme I, but had an altered pattern of activity when amylose was used as substrate. In addition to the typical fall in absorbance at high wavelengths (500-700 nm) of the amylose-I complex, branching of amylose of sugary branching enzyme I caused an increase in absorbance at low wavelengths (400-550 nm). Branching enzyme IIb was undetected in exts. of amylose-extender kernels, whereas branching enzymes I and IIa appeared unaltered. Low unprimed starch synthase activity was also observed in DEAE-cellulose fractions of amylose-extender maize, but this activity was regenerated by the addition of any branching enzyme.

AN 1978:85042 HCAPLUS <<LOGINID::20100610>>

DN 88:85042

OREF 88:13337a,13340a

TI Multiple forms of starch branching enzyme of maize: evidence for independent genetic control

AU Boyer, Charles D.; Preiss, Jack

CS Dep. Biochem. Biophys., Univ. California, Davis, CA, USA

SO Biochemical and Biophysical Research Communications (1978), 80(1), 169-75
CODEN: BBRCA9; ISSN: 0006-291X

DT Journal

LA English

OSC.G 45 THERE ARE 45 CAPLUS RECORDS THAT CITE THIS RECORD (45 CITINGS)

L8 ANSWER 70 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Interaction of the amylose-extender and waxy mutants of maize

AB The interaction of the amylose-extender (ae) and way (wx) mutants of corn was studied by determination of changes in kernel dry weight, endosperm starch, and apparent amylose (percent) during development of the 16 genotypes involving the complete dosage series for the 2 loci. Increasing doses of the recessive wx allele from 0 to 3 had no effect on kernel dry weight, except when the mutant dose at the ae locus was 3. Similarly, increasing doses of the wx allele did not decrease endosperm starch until the mutant background dosage at the ae locus was 2 or 3. In contrast, increasing doses of the recessive ae allele decreased kernel dry weight and endosperm starch, regardless of the gene dosage at the wx locus. Increasing dosage at both loci had definite effects on apparent amylose content, although single doses of the recessive allele at either locus were not significantly different from no recessive alleles. Two or 3 doses of the wx allele significantly decreased apparent amylose, while 2 or 3 doses of the ae allele significantly increased apparent amylose, regardless of the gene dosage at the other locus. Based on these data and other information in the literature it is proposed that the gene product of the Ae allele controls the quantity of an effector, possibly citrate, which stabilizes a branching enzyme-starch synthetase complex. Thus, the enzyme complex is necessary for normal amylopectin production

AN 1976:574400 HCAPLUS <<LOGINID::20100610>>

DN 85:174400

OREF 85:27869a,27872a

TI Interaction of the amylose-extender and waxy mutants of maize

AU Boyer, C. D.; Garwood, D. L.; Shannon, J. C.

CS Dep. Hortic., Pennsylvania State Univ., University Park, PA, USA

SO Journal of Heredity (1976), 67(4), 209-14
CODEN: JOHEA8; ISSN: 0022-1503

DT Journal
LA English
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)

L8 ANSWER 71 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Starch synthetases from Vitis vinifera and Zea mays
AB ADP glucose: α-1,4-glucan α-4-glucosyltransferases (starch synthetases) [9030-10-8] from leaves of V. vnifera and leaves and kernels of Z. mays were chromatographed on DEAE-cellulose columns. ADP glucose: α-1,4-glucan α-4-glucosyltransferases (starch synthetases) [9030-10-8] from leaves of V. vinifera and leaves and kernels of Z. mays were chromatographed on DEAE-cellulose columns. One form of the enzyme was present in grape leaves having activity both in the presence and absence of primer. Two forms were present in both leaves and kernels of maize. The second peak of activity in maize leaves and the first peak in maize kernels synthesized a polyglucan in the absence of primer. A peak of branching enzyme (Q-enzyme) [9001-97-2] occurred between the 2 starch synthetase peaks with both tissues. When fractions containing starch synthetase and branching enzyme were added to the first leaf starch synthetase peak, up to 100-fold activation of the unprimed reaction occurred. Branching enzyme did not stimulate the unprimed activity of the first kernel peak and no branching enzyme could be detected in this peak. The unprimed product was a branched polyglucan with mainly α-1,4-links.
AN 1974:459891 HCAPLUS <<LOGINID::20100610>>
DN 81:59891
OREF 81:9535a,9538a
TI Starch synthetases from Vitis vinifera and Zea mays
AU Hawker, John S.; Downton, John S.
CS Div. Hortic. Res., CSIRO, Adelaide, Australia
SO Phytochemistry (Elsevier) (1974), 13(6), 893-900
CODEN: PYTCAS; ISSN: 0031-9422
DT Journal
LA English
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

=> d his

(FILE 'HOME' ENTERED AT 13:42:08 ON 10 JUN 2010)

FILE 'HCAPLUS' ENTERED AT 13:42:39 ON 10 JUN 2010
L1 1369 S BRANCHING ENZYME
L2 44820 S MAIZE
L3 263 S L1 AND L2
L4 96 S L3 AND (PY<2000 OR AY<2000 OR PRY<2000)
L5 808 S (BRANCHING ENZYME)(4A)(STARCH)
L6 851 S (BRANCHING ENZYME)(4A)(STARCH OR AMYLOSE OR AMYLOPECTIN)
L7 231 S L2 AND L6
L8 71 S L7 AND (PY<2000 OR AY<2000 OR PRY<2000)

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PASSWORD:
 * * * * * * RECONNECTED TO STN INTERNATIONAL * * * * * *
SESSION RESUMED IN FILE 'HCAPLUS' AT 14:32:30 ON 10 JUN 2010
FILE 'HCAPLUS' ENTERED AT 14:32:30 ON 10 JUN 2010
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COST IN U.S. DOLLARS                            SINCE FILE      TOTAL
                                                   ENTRY    SESSION
FULL ESTIMATED COST                                228.14     228.36

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)      SINCE FILE      TOTAL
                                                   ENTRY    SESSION
CA SUBSCRIBER PRICE                                -58.65     -58.65

=> s expression or expressed or (degree of branching) or (branching degree) or
isolated or isolation or purified
       1251007 EXPRESSION
        565632 EXPRESSED
       4754868 DEGREE
         65463 BRANCHING
          2426 DEGREE OF BRANCHING
               (DEGREE(1W)BRANCHING)
         65463 BRANCHING
       4754868 DEGREE
           529 BRANCHING DEGREE
               (BRANCHING(W)DEGREE)
        971851 ISOLATED
        302919 ISOLATION
        479673 PURIFIED
L9     2911043 EXPRESSION OR EXPRESSED OR (DEGREE OF BRANCHING) OR (BRANCHING
               DEGREE) OR ISOLATED OR ISOLATION OR PURIFIED

=> s l8 and l9
L10          60 L8 AND L9

=> s expression or expressed or (degree of branching) or (branching degree)
       1251007 EXPRESSION
        565632 EXPRESSED
       4754868 DEGREE
         65463 BRANCHING
          2426 DEGREE OF BRANCHING
               (DEGREE(1W)BRANCHING)
         65463 BRANCHING
       4754868 DEGREE
           529 BRANCHING DEGREE
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L11    1540936 EXPRESSION OR EXPRESSED OR (DEGREE OF BRANCHING) OR (BRANCHING
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=> s l8 and l11
L12          33 L8 AND L11

=> d l12 1-33 ti abs bib

L12  ANSWER 1 OF 33  HCAPLUS  COPYRIGHT 2010 ACS on STN
TI   Protein and cDNA sequences of corn gene dull1 coding for a starch synthase
     and use
AB   The maize gene dull1 (dul) of the present invention is a
     determinant of the structure of endosperm starch.  Mutations of dul affect
     the activity of at least two enzymes involved in starch biosynthesis,
     namely the starch synthase, SSII, and the starch
     branching enzyme, SBEIIa.  Dul codes for a predicted
     1674 residue protein, and is expressed with a unique temporal
     pattern in endosperm but is undetectable in leaf or root.  The size of the
     Dul product and its expression pattern match precisely the known
     characteristics of maize SSII.  The Dul product contains two
     different repeated regions in its unique amino terminus, one of which is
     identical to a conserved segment of the starch debranching enzymes.  The
     cDNA provided for in the present invention encodes SSII, and mutations
     within this gene affect multiple aspects of starch biogenesis by
     disrupting an enzyme complex containing starch synthase(s),
     starch branching enzyme(s), and possibly
     starch debranching enzyme.
AN   2003:851297  HCAPLUS <<LOGINID::20100610>>
DN   139:334824
TI   Protein and cDNA sequences of corn gene dull1 coding for a starch synthase
     and use
IN   Myers, Alan M.; James, Martha Graham
PA   Iowa State University Research Foundation, Inc., USA
SO   U.S., 56 pp., Cont.-in-part of U.S. Ser. No. 968,542.
     CODEN: USXXAM
DT   Patent
LA   English
FAN.CNT 2
     PATENT NO.          KIND   DATE        APPLICATION NO.        DATE
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PI   US 6639125           B1    20031028    US 2000-554467         20000512 <--
     US 5981728           A     19991109    US 1997-968542         19971112 <--
     WO 9924575           A1    19990520    WO 1998-US24225        19981112 <--
         W:  AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE,
             ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS,
             LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD,
             SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN
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             CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     US 20040049810       A1    20040311    US 2003-634262         20030805 <--
PRAI US 1997-968542       A2    19971112  <--
     WO 1998-US24225      W     19981112  <--
     US 2000-554467       A1    20000512
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G   1     THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT  16    THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12  ANSWER 2 OF 33  HCAPLUS  COPYRIGHT 2010 ACS on STN
TI   The rice actin 2 promoter and intron and their use for plant
     transformation
AB   The current invention provides regulatory regions from the rice actin 2
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gene. In particular, the current invention provides the rice actin 2 promoter and actin 2 intron. Compns. comprising these sequences are described, as well as transformation constructs derived therefrom. Further provided are methods for the expression of transgenes in plants comprising the use of these sequences. The methods of the invention include the direct creation of transgenic plants with the rice actin 2 intron and/or promoter directly by genetic transformation, as well as by plant breeding methods. The actin 2 sequences of the invention represent a valuable new tool for the creation of transgenic plants, preferably having one or more added beneficial characteristics.

AN 2000:824429 HCAPLUS <<LOGINID::20100610>>
DN 133:359795
TI The rice actin 2 promoter and intron and their use for plant transformation
IN McElroy, David; Wu, Ray
PA Dekalb Genetics Corporation, USA; Cornell Research Foundation, Inc.
SO PCT Int. Appl., 180 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000070067	A1	20001123	WO 2000-US13303	20000512 <--
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	US 6429357	B1	20020806	US 1999-312304	19990514 <--
	CA 2372859	A1	20001123	CA 2000-2372859	20000512 <--
	EP 1179081	A1	20020213	EP 2000-942636	20000512 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	EP 2123764	A1	20091125	EP 2009-169512	20000512 <--
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PRAI	US 1999-312304	A1	19990514 <--		
	EP 2000-942636	A3	20000512		
	WO 2000-US13303	W	20000512		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 3 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Biosynthesis of altered starch in genetically modified plants with glycogen branching enzyme gene
AB A method and compns. for altering starch properties in wheat and maize plants, starch obtained by such method, and transgenic plants producing such starch, are disclosed. Starch with altered properties is produced by introducing a gene construct comprising a glycogen branching enzyme coding sequence under the control of a promoter directing expression and a terminator. A transit peptide for translocation of the glycogen branching enzyme to the plant plastid may also be included in the chimeric gene construct. The starch has altered processing characteristics, in particular an decreased chain length. A chimeric gene containing the High Mol. Weight Glutenin (HMWG) promoter, nopaline

synthase terminator, and the transit-peptide region of the small-subunit of the ribulose bisphosphate carboxylase (ssu of Rubisco) gene was utilized to direct expression of Escherichia coli glycogen branching enzyme (glgB) to wheat and maize. Expression of the glgB gene product in wheat and maize grain was detected by immunoblot anal. Anal. of the starch from these transgenic wheat and maize lines indicated an decrease in chain length, particularly an increase in chain length between 5 and 8 glucose units. The above parameters indicate a novel wheat and maize starch based on expression of the glgB E. coli gene product in transgenic plants.

AN 2000:368616 HCAPLUS <<LOGINID::20100610>>
DN 133:29689
TI Biosynthesis of altered starch in genetically modified plants with glycogen branching enzyme gene
IN Burrell, Michael Meyrick
PA Advanced Technologies (Cambridge) Limited, UK
SO PCT Int. Appl., 56 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000031282	A1	20000602	WO 1999-GB3762	19991108 <--

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI GB 1998-25262 A 19981119 <--
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 4 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Biosynthesis of altered starch in genetically modified plants with glycogen synthase gene
AB A method and compns. for altering starch properties in wheat and maize plants , starch obtained by such method, and transgenic plants producing such starch, are disclosed. Starch with altered properties is produced by introducing a gene construct comprising a glycogen synthase coding sequence under the control of a promoter directing expression and a terminator. A transit peptide for translocation of the glycogen synthase to the plant plastid may also be included in the chimeric gene construct. The starch has altered processing characteristics, in particular an increased chain length. A chimeric gene containing the High Mol. Weight Glutenin (HMWG) promoter, nopaline synthase terminator, and the transit-peptide region of the small-subunit of the ribulose bisphosphate carboxylase (ssu of Rubisco) gene was utilized to direct expression of Escherichia coli glycogen synthase (glgA) to wheat and maize. Expression of the glgA gene product in wheat and maize grain was detected by immunoblot anal. Anal. of the starch from these transgenic wheat and maize lines indicated an increase in chain length, particularly in chain length between 17 and 28 glucose units. Rapid viscometric anal. yielded lower peak and final viscosity values (about 30% of control values), whereas differential scanning calorimetry values indicated

increased enthalpy values. The above parameters indicate a novel wheat and maize starch based on expression of the glgA E. coli gene product in transgenic plants.

AN 2000:368603 HCAPLUS <<LOGINID::20100610>>

DN 133:29688

TI Biosynthesis of altered starch in genetically modified plants with glycogen synthase gene

IN Burrell, Michael Meyrick

PA Advanced Technologies (Cambridge) Limited, UK

SO PCT Int. Appl., 66 pp.
CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 2000031274	A1	20000602	WO 1999-GB3734	19991109	<--
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	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG					
	CA 2349819	A1	20000602	CA 1999-2349819	19991109	<--
	CA 2349819	C	20080909			
	EP 1131442	A1	20010912	EP 1999-954197	19991109	<--
	EP 1131442	B1	20100526			
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, CY					
	US 6468799	B1	20021022	US 1999-444728	19991118	<--
	AU 2000010616	A	20000807	AU 2000-10616	20000119	<--
	AU 2004202150	A1	20040617	AU 2004-202150	20040519	
	AU 2004202150	B2	20060713			
PRAI	GB 1998-25242	A	19981119	<--		
	WO 1999-GB3734	W	19991109	<--		
	AU 2000-10616	A3	20000119			

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 5 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Starch branching enzyme II (SBEII-1 and SBEII-2) isoforms from wheat, cDNA, transgenic plants, and altering starch properties for food use

AB A class of wheat SBEII genes, SBEII-1, recombinant protein expression in transgenic plants, and its use in altering properties of starch produced by a plant are claimed. Starch properties include the gelatinization onset and/or peak temperature The use of such starch with altered properties in food stuff, particularly bakery products is also claimed. CDNA clones for SBEII were isolated and sequenced. Those clones were divided into two sub-classes, SBEII-1 and SBEII-2 having sequence homol. to maize SBEIIb and SBEIIa, resp. These genes were mapped to the long arm of wheat group 2 homologous chromosomes. Some of those isoforms were expressed as recombinant protein in wheat. Differential scanning calorimetry studies showed that starch produced in transgenic wheat transformed with expression construct for SBEII displayed higher onset, peak, and end temperature for

gelatinization.
AN 2000:191230 HCAPLUS <<LOGINID::20100610>>
DN 132:247996
TI Starch branching enzyme II (SBEII-1 and SBEII-2) isoforms from wheat, cDNA, transgenic plants, and altering starch properties for food use
IN Goldsbrough, Andrew; Colliver, Steve
PA Plant Breeding International Cambridge Ltd., UK
SO PCT Int. Appl., 198 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 2000015810	A1	20000323	WO 1999-GB3011	19990909	<--
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	AU 9958725	A	20000403	AU 1999-58725	19990909	<--
	AU 767103	B2	20031030			
	EP 1117814	A1	20010725	EP 1999-946307	19990909	<--
	EP 1117814	B1	20100217			
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, CY					
	HU 2001003618	A2	20020128	HU 2001-3618	19990909	<--
	HU 2001003618	A3	20031229			
	AT 458061	T	20100315	AT 1999-946307	19990909	<--
	US 6730825	B1	20040504	US 2001-786480	20010917	<--
	US 20040216188	A1	20041028	US 2004-818770	20040406	<--
	US 7217857	B2	20070515			
	US 20080064864	A1	20080313	US 2007-788837	20070419	<--
	US 7465851	B2	20081216			
PRAI	EP 1998-307337	A	19980910	<--		
	WO 1999-GB3011	W	19990909	<--		
	US 2001-786480	A3	20010917			
	US 2004-818770	A3	20040406			

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 6 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Expression control elements from the 5'- and 3'-regions of genes for starch branching enzymes
AB Regulatory elements from the 5'- and 3'-flanking regions of maize genes for starch branching enzymes (SbeI and Ae) are described for use in the expression of foreign genes in transgenic plants. The genes show different patterns of expression in tissues of the seed during its development and so the regulatory elements may be of use in the regulation of foreign gene expression in cereals. The genes were cloned by screening a genomic library with PCR products. The SbeI gene has a perfectly palindromic G-box in the promoter region while the Ae gene had elements resembling metal responsive elements, GC boxes, Hex, and I boxes. Functional anal. of the SbeI promoter identified sequences responsible for high level transcription and sugar regulation of gene

expression. It also showed that elements within the transcribed region play a role in high level gene expression and that there sequences in the 5'-region that limit gene expression. An essential region of 60 bp was identified and shown to bind DNA-binding proteins.

AN 1999:795936 HCAPLUS <<LOGINID::20100610>>
DN 132:31802
TI Expression control elements from the 5'- and 3'-regions of genes for starch branching enzymes
IN Guiltinan, Mark J.; Kim, Kyung-Nam
PA The Pennsylvania State University, USA
SO PCT Int. Appl., 110 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9964562	A2	19991216	WO 1999-US13266	19990611 <--
WO 9964562	A3	20000518		
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9944384	A	19991230	AU 1999-44384	19990611 <--
PRAI US 1998-89049P	P	19980612	<--	
US 1998-89050P	P	19980612	<--	
WO 1999-US13266	W	19990611	<--	

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 7 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Carbon isotope ratios of amylose, amylopectin and mutant starches
AB Carbon isotope ratios (expressed as δ13C values) were determined for various sources of starch and the starch fractions amylose and amylopectin. The δ13C values of amylose were consistently less neg., 0.4-2.3.permill., than those of amylopectin in kernel starch from maize (Zea mays) and barley (Hordeum vulgare) and in tuber starch from potato (Solanum tuberosum). Kernel starch isolated from the maize mutants wx1 and ae1, with known genetic lesions in the starch biosynthetic pathway, also showed significant differences in δ13C values. Collectively, these results suggest that variation in carbon isotope ratios in the amylose and amylopectin components of starch may be attributed to isotopic discrimination by the enzymes involved in starch biosynthesis.
AN 1999:737017 HCAPLUS <<LOGINID::20100610>>
DN 132:76065
TI Carbon isotope ratios of amylose, amylopectin and mutant starches
AU Scott, M. Paul; Jane, Jay-Lin; Soundararajan, Madhavan
CS USDA-ARS, Department of Agronomy, Iowa State University, Ames, IA, 50011, USA
SO Phytochemistry (1999), 52(4), 555-559
CODEN: PYTCAS; ISSN: 0031-9422
PB Elsevier Science Ltd.
DT Journal
LA English
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 8 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Expression of transgenes in plants using promoter and terminator sequences from Coix
AB Methods and compns. for the expression of transgenes in monocot plants including maize are disclosed. In the invention, gene silencing is avoided by use of monocot-homeologous sequences from plants of the genus Coix for transformation. Included in these transgene sequences are Coix promoters, enhancers, coding sequences and terminators. Suitable alternatives to maize-derived transgenes are desirable for expression in maize in that homol.-based gene silencing can limit or effectively eliminate transgene expression .
AN 1999:736897 HCAPLUS <<LOGINID::20100610>>
DN 131:347500
TI Expression of transgenes in plants using promoter and terminator sequences from Coix
IN Kriz, Alan L.; Luethy, Michael H.; Voyles, Dale A.
PA Dekalb Genetics Corporation, USA
SO PCT Int. Appl., 240 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9958659	A2	19991118	WO 1999-US10776	19990514 <--
	WO 9958659	A3	20000120		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 6635806	B1	20031021	US 1998-78972	19980514 <--
	CA 2328129	A1	19991118	CA 1999-2328129	19990514 <--
	AU 9939957	A	19991129	AU 1999-39957	19990514 <--
	EP 1076706	A2	20010221	EP 1999-923112	19990514 <--
	EP 1076706	B1	20080206		
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	TR 2001000104	T2	20010621	TR 2001-104	19990514 <--
	BR 9910455	A	20011127	BR 1999-10455	19990514 <--
	JP 2002533057	T	20021008	JP 2000-548450	19990514 <--
	AT 385518	T	20080215	AT 1999-923112	19990514 <--
	PT 1076706	E	20080509	PT 1999-923112	19990514 <--
	ES 2301239	T3	20080616	ES 1999-923112	19990514 <--
	IN 2000DN00321	A	20080620	IN 2000-DN321	20001109 <--
	IN 227562	A1	20090130		
	ZA 2000006576	A	20020213	ZA 2000-6576	20001113 <--
	MX 2000011199	A	20010419	MX 2000-11199	20001114 <--
	US 20050250938	A1	20051110	US 2003-660097	20030911 <--
	US 7256283	B2	20070814		
	IN 2005DN05625	A	20070928	IN 2005-DN5625	20051205 <--
	US 20080271212	A1	20081030	US 2007-838724	20070814 <--
	US 20090013423	A1	20090108	US 2007-838725	20070814 <--
	US 20090199307	A1	20090806	US 2007-838721	20070814 <--

PRAI US 1998-78972 A1 19980514 <--
WO 1999-US10776 W 19990514 <--
IN 2000-DN321 A3 20001109
US 2003-660097 A3 20030911
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 9 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Identification of cis-acting elements important for expression of the starch-branching enzyme I gene in maize endosperm
AB The genes encoding the starch-branching enzymes (SBE) SBEI, SBEIIa, and SBEIIb in maize (Zea mays) are differentially regulated in tissue specificity and during kernel development. To gain insight into the regulatory mechanisms controlling their expression, we analyzed the 5'-flanking sequences of Sbe1 using a transient gene expression system. Although the 2.2-kb 5'-flanking sequence between -2,190 and +27 relative to the transcription initiation site was sufficient to promote transcription, the addition of the transcribed region between +28 and +228 containing the first exon and intron resulted in high-level expression in suspension-cultured maize endosperm cells. A series of 5' deletion and linker-substitution mutants identified two critical pos. cis elements, -314 to -295 and -284 to -255. An electrophoretic mobility-shift assay showed that nuclear proteins prepared from maize kernels interact with the 60-bp fragment containing these two elements. Expression of the Sbe1 gene is regulated by sugar concentration in suspension-cultured maize endosperm cells, and the region -314 to -145 is essential for this effect. Interestingly, the expression of mEmBP-1, a bZIP transcription activator, in suspension-cultured maize endosperm cells resulted in a 5-fold decrease in Sbe1 promoter activity, suggesting a possible regulatory role of the G-box present in the Sbe1 promoter from -227 to -220.
AN 1999:615638 HCAPLUS <<LOGINID::20100610>>
DN 132:815
TI Identification of cis-acting elements important for expression of the starch-branching enzyme I gene in maize endosperm
AU Kim, Kyung-Nam; Guiltinan, Mark J.
CS Intercollege Graduate Program in Plant Physiology, The Biotechnology Institute, and Department of Horticulture, The Pennsylvania State University, University Park, PA, 16802, USA
SO Plant Physiology (1999), 121(1), 225-236
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
OSC.G 17 THERE ARE 17 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)
RE.CNT 65 THERE ARE 65 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 10 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Maize starch synthase gene du1 and uses in starch production
AB Disclosed are the maize du1 gene, the encoded starch synthase isoenzyme II, and production of starch with recombinant du1-expressing cells or transgenic plants. The maize gene dull1 (du1) of the present invention is a determinant of the structure of endosperm starch. Mutations of du1 affect the activity of at least two enzymes involved in starch biosynthesis, namely the starch synthase, SSII, and the starch branching enzyme, SBEIIa. Du1 codes

for a predicted 1674 residue protein, and is expressed with a unique temporal pattern in endosperm but is undetectable in leaf or root. The size of the Du1 product and its expression pattern match precisely the known characteristics of maize SSII. The Du1 product contains two different repeated regions in its unique amino terminus, one of which is identical to a conserved segment of the starch debranching enzymes. The cDNA provided for in the present invention encodes SSII, and mutations within this gene affect multiple aspects of starch biogenesis by disrupting an enzyme complex containing starch synthase(s), starch branching enzyme(s), and possibly starch debranching enzyme(s).

AN 1999:326050 HCAPLUS <<LOGINID::20100610>>
DN 130:333760
TI Maize starch synthase gene du1 and uses in starch production
IN Myers, Alan M.; James, Martha G.
PA Iowa State University Research Foundation, Inc., USA
SO PCT Int. Appl., 138 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9924575	A1	19990520	WO 1998-US24225	19981112	<--
	W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN					
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG					
	US 5981728	A	19991109	US 1997-968542	19971112	<--
	CA 2309346	A1	19990520	CA 1998-2309346	19981112	<--
	AU 9915236	A	19990531	AU 1999-15236	19981112	<--
	AU 761419	B2	20030605			
	EP 1030922	A1	20000830	EP 1998-959440	19981112	<--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI					
	BR 9814864	A	20011106	BR 1998-14864	19981112	<--
	JP 2001522604	T	20011120	JP 2000-520569	19981112	<--
	NZ 504534	A	20021220	NZ 1998-504534	19981112	<--
	MX 2000004586	A	20001110	MX 2000-4586	20000512	<--
	US 6639125	B1	20031028	US 2000-554467	20000512	<--
PRAI	US 1997-968542	A	19971112	<--		
	WO 1998-US24225	W	19981112	<--		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 11 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Characterization of a gene encoding wheat endosperm starch branching enzyme-I
AB A genomic DNA fragment from Triticum tauschii, the donor of the wheat D genome, contains a starch branching enzyme-I (SBE-I) gene spread over 6.5 kb. This gene (designated wSBE I-D4) encodes an amino acid sequence identical to that determined for the N-terminus of SBE-I from the hexaploid wheat (T. aestivum) endosperm. Cognate cDNA sequences for wSBE I-D4 were isolated from hexaploid wheat by hybridization screening from an endosperm library and also by PCR. A contiguous sequence (D4 cDNA) was assembled from the sequence of five overlapping

partial cDNAs which spanned wSBE I-D4. D4 cDNA encodes a mature polypeptide of 87 kDa that shows 90% identity to SBE-I amino acid sequences from rice and maize and contains all the residues considered essential for activity. D4 mRNA has been detected only in the endosperm and is at a maximum concentration mid-way through grain development. The wSBE I-D4 gene consists of 14 exons, similar to the structure for the equivalent gene in rice; the rice gene has a strikingly longer intron 2. The 3' end of wSBE I-D4 was used to show that the gene is located on group 7 chromosomes. The sequence upstream of wSBE I-D4 was analyzed with respect to conserved motifs.

AN 1999:177589 HCAPLUS <<LOGINID::20100610>>
DN 131:83671
TI Characterization of a gene encoding wheat endosperm starch branching enzyme-I
AU Rahman, S.; Li, Z.; Abrahams, S.; Abbott, D.; Appels, R.; Morell, M. K.
CS CSIRO Plant Industry, Canberra, 2601, Australia
SO Theoretical and Applied Genetics (1999), 98(1), 156-163
CODEN: THAGA6; ISSN: 0040-5752
PB Springer-Verlag
DT Journal
LA English
OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 12 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Molecular cloning and characterization of the Amylose-Extender gene encoding starch branching enzyme IIB in maize
AB The amylose-extender (Ae) gene encoding starch-branching enzyme IIb (SBEIIb) in maize is predominantly expressed in endosperm and embryos during kernel development. A maize genomic DNA fragment (-2964 to +20485) containing the Ae gene was isolated and sequenced. The maize Ae mRNA is derived from 22 exons distributed over 16914 bp. Twenty-one introns, differing in length from 76 bp to 4020 bp, all have conserved junction sequences (GT··AG). Sequence anal. of the 5'- and 3'-flanking regions revealed a consensus TATA-box sequence located 28 bp upstream of the transcription initiation site as determined by primer extension anal., and a putative polyadenylation signal observed 29 bp upstream of the polyadenylation site based on cDNA sequence. Genomic Southern blot anal. suggests that a single Ae gene is present in the maize genome. Promoter activity was confirmed by testing a transcriptional fusion of the Ae 5'-flanking region between -2964 and +100 to a luciferase reporter gene in a transient expression assay using maize endosperm suspension cultured cells. 5' deletion anal. revealed that the 111 bp region from -160 to -50 is essential for high-level promoter activity.
AN 1999:44300 HCAPLUS <<LOGINID::20100610>>
DN 130:219005
TI Molecular cloning and characterization of the Amylose-Extender gene encoding starch branching enzyme IIB in maize
AU Kim, Kyung-Nam; Fisher, Dane K.; Gao, Ming; Guiltinan, Mark J.
CS Intercollege Graduate Programs in Plant Physiology and Genetics, The Biotechnology Institute, and Department of Horticulture, The Pennsylvania State University, University Park, PA, 16802, USA
SO Plant Molecular Biology (1998), 38(6), 945-956
CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer Academic Publishers
DT Journal

LA English
OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 13 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Manipulating the starch composition of potato
AB A review with 41 refs. Starch can be fractionated into two types of glucose polymers: amylose and amylopectin. Amylose consists of essentially linear chains of α-(1,4)-linked glucose residues, whereas amylopectin is built up from α-(1,4)-linked chains with α-(1,6)-linked branches. The composition and fine structure of starch are responsible for many of the physicochem. properties and thus dets. its industrial uses. Variation in starch structure and composition can be found between and within crops. In the latter case it can be found in mutants, often resulting from the loss of function of one or more of the genes involved in starch biosynthesis. In maize, the most extensively studied crop, mutant genotypes are known for nearly every gene identified as being involved in starch biosynthesis. Differences in starch composition can also be achieved by genetic modifications such as antisense inhibition of genes or overexpression of (heterologous) genes. Most examples of genetic modification of starch composition are in potato, which can easily be transformed. Antisense inhibition of enzymes in the biosynthetic pathway, such as ADP glucose phosphorylase (AGP), (granule-bound) starch synthase or branching enzyme, lead to an altered starch content and/or composition In addition, the introduction and expression of bacterial genes, such as genes of the Escherichia coli glycogen synthesis pathway, in potato leads to starches with altered content, composition, structure and physicochem. properties. Studying the physicochem. properties of these altered starches will, together with the information obtained by research on starches of mutants, help to clarify the precise relationship between structural and functional features of starch.
AN 1998:787972 HCAPLUS <<LOGINID::20100610>>
DN 130:165463
TI Manipulating the starch composition of potato
AU Kortstee, A. J.; Flipse, E.; Kuipers, A. G. J.; Jacobsen, E.; Visser, R. G. F.
CS Graduate School of Experimental Plant Sciences, Department of Plant Breeding, Agricultural University Wageningen, Wageningen, 6700 AJ, Neth.
SO Portland Press Proceedings (1998), 14(Engineeering Crop Plants for Industrial End Uses), 89-98
CODEN: POPPEF; ISSN: 0966-4068
PB Portland Press Ltd.
DT Journal; General Review
LA English
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 14 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Analysis of essential histidine residues of maize branching enzymes by chemical modification and site-directed mutagenesis
AB Incubation of maize branching enzyme, mBEI and mBEII, with 100 μM diethylpyrocarbonate (DEPC) rapidly inactivated the enzymes. Treatment of the DEPC-inactivated enzymes with 100-500 mM hydroxylamine restored the enzyme activities. Spectroscopic data indicated that the inactivation of BE with DEPC was the result of histidine modification. The addition of the substrate amylose or amylopectin retarded the enzyme inactivation by DEPC, suggesting that the histidine residues are important for substrate binding. In maize BEII, conserved histidine

residues are in catalytic regions 1 (His320) and 4 (His508). His320 and His508 were individually replaced by Ala via site-directed mutagenesis to probe their role in catalysis. Expression of these mutants in E. coli showed a significant decrease of the activity and the mutant enzymes had Km values 10 times higher than the wild type. Therefore, residues His320 and His508 do play an important role in substrate binding.
AN 1998:784558 HCAPLUS <<LOGINID::20100610>>
DN 130:121357
TI Analysis of essential histidine residues of maize branching enzymes by chemical modification and site-directed mutagenesis
AU Funane, Kazumi; Libessart, Nathalie; Stewart, Douglas; Michishita, Toru; Preiss, Jack
CS Department of Biochemistry, Michigan State University, East Lansing, MI, 48824, USA
SO Journal of Protein Chemistry (1998), 17(7), 579-590
CODEN: JPCHD2; ISSN: 0277-8033
PB Plenum Publishing Corp.
DT Journal
LA English
OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)
RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 15 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Genomic organization and promoter activity of the maize starch branching enzyme I gene
AB Starch branching enzymes (SBE) which catalyze the formation of α-1,6-glucan linkages are of crucial importance for the quantity and quality of starch synthesized in plants. In maize (Zea mays L.), three SBE isoforms (SBEI, IIa and IIb) have been identified and shown to exhibit differential expression patterns. As a first step toward understanding the regulatory mechanisms controlling their expression, the authors isolated and sequenced a maize genomic DNA (-2190 to +5929) which contains the entire coding region of SBEI (Sbe1) as well as 5'-and 3'-flanking sequences. Using this clone, the authors established a complete genomic organization of the maize Sbe1 gene. The transcribed region consists of 14 exons and 13 introns, distributed over 5.7 kb. A consensus TATA-box and a G-box containing a perfect palindromic sequence, CCACGTGG, were found in the 5'-flanking region. Genomic Southern blot anal. indicated that two Sbe1 genes with divergent 5'-flanking sequences exist in the maize genome, suggesting the possibility that they are differentially regulated. A chimeric construct containing the 5'-flanking region of Sbe1 (-2190 to +27) fused to the β-glucuronidase gene (pKG101) showed promoter activity after it was introduced into maize endosperm suspension cells by particle bombardment.
AN 1998:597027 HCAPLUS <<LOGINID::20100610>>
DN 129:311547
OREF 129:63465a,63468a
TI Genomic organization and promoter activity of the maize starch branching enzyme I gene
AU Kim, Kyung-Nam; Fisher, Dane K.; Gao, Ming; Guiltinan, Mark J.
CS Intercollege Graduate Programs in Plant Physiology and Genetics, Biotechnology Institute, Dep. Horticulture, Pennsylvania State University, Pennsylvania, PA, 16802, USA
SO Gene (1998), 216(2), 233-243
CODEN: GENED6; ISSN: 0378-1119
PB Elsevier Science B.V.
DT Journal
LA English
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)

RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 16 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Altering starch structure and functionality by manipulating expression of starch biosynthetic enzymes.
AB Starch functionality is a product of the fine structure of a given starch polymer. This structure is a result of the concerted action of several starch synthases, starch branching enzymes and starch debranching enzymes. To examine the relationship between starch polymer structure and starch functionality we are using transgenic approaches to control the expression of genes encoding starch biosynthetic enzymes and examine the impacts of altered gene expression on starch structure and functionality. We have isoalted and characterized maize cDNAs encoding Starch Branching Enzymes I and IIb (SBE I SBEIIb) and generated transgenic maize plants carrying constructions for under and over expression of these two genes. The effects of altered branching enzyme expression on starch polymer structure and starch functionality will be presented.
AN 1998:530122 HCAPLUS <<LOGINID::20100610>>
TI Altering starch structure and functionality by manipulating expression of starch biosynthetic enzymes.
AU Lightner, Jonathan; Broglie, Karen; Cressman, Robert; Hines, Chris; Pearlstein, Rich; Hubbard, Natalie
CS Stine-Haskell Research Center, DuPont Agricultural Products, Newark, DE, 19714-0030, USA
SO Book of Abstracts, 216th ACS National Meeting, Boston, August 23-27 (1998), AGFD-137 Publisher: American Chemical Society, Washington, D. C.
CODEN: 66KYA2
DT Conference; Meeting Abstract
LA English

L12 ANSWER 17 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Starch granule-associated protein and transgenic plants producing starch with altered viscosity and phosphate content
AB Nucleic acid mols. are described encoding a starch granule-bound protein from potato and maize as well as methods and recombinant DNA mols. for the production of transgenic plant cells and plants synthesizing a modified starch. Potato and maize cDNAs for a starch granule-associated protein were cloned and sequenced. Transgenic potatoes expressing an antisense version of the potato cDNA produced starch with .apprx.50% lower phosphate content and with altered gelling properties. When the starch granule-associated protein cDNA was expressed in Escherichia coli, glycogen with higher than normal phosphate content was produced.
AN 1998:424347 HCAPLUS <<LOGINID::20100610>>
DN 129:91420
OREF 129:18743a,18746a
TI Starch granule-associated protein and transgenic plants producing starch with altered viscosity and phosphate content
IN Kossmann, Jens; Emmermann, Michael
PA Planttec Biotechnologie G.m.b.H., Germany
SO PCT Int. Appl., 123 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

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PI   WO 9827212          A1    19980625    WO 1997-EP7123         19971218 <--
        W:  AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,
            DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG,
            KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX,
            NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,
            UA, UG, US, UZ, VN, YU, ZW
        RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI,
            FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM,
            GA, GN, ML, MR, NE, SN, TD, TG
     DE 19653176           A1    19980625    DE 1996-19653176       19961219 <--
     CA 2272844            A1    19980625    CA 1997-2272844        19971218 <--
     AU 9858577            A     19980715    AU 1998-58577          19971218 <--
     AU 740492             B2    20011108
     EP 950107             A1    19991020    EP 1997-954424         19971218 <--
     EP 950107             B1    20070321
        R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, NL, SE, PT
     JP 2001522223         T     20011113    JP 1998-527334         19971218 <--
     JP 4098365            B2    20080611
     AT 357522             T     20070415    AT 1997-954424         19971218 <--
     PT 950107             E     20070531    PT 1997-954424         19971218 <--
     ES 2280086            T3    20070901    ES 1997-954424         19971218 <--
     US 7186898            B1    20070306    US 1999-334103         19990616 <--
PRAI DE 1996-19653176      A     19961219  <--
     WO 1997-EP7123        W     19971218  <--
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G   9     THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)
RE.CNT  4     THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12  ANSWER 18 OF 33  HCAPLUS  COPYRIGHT 2010 ACS on STN
TI   Promoter of wheat wbeI gene for expressing foreign genes in
     monocotyledonous plants
AB   A DNA fragment for directing the expression of foreign or
     endogenous genes or RNA in cells of monocot plants.  The fragment
     comprises a sequence corresponding to a first part of a putative type I
     starch branching enzyme gene (wbeI) present in
     wheat and a 5'-region upstream of the gene, or a part of the sequence that
     is effective for increasing the expression of the foreign or
     endogenous gene in the plant cells.  The indicated sequence contains two
     promoter regions, P1 and P2.  A DNA fragment effective to increase
     expression comprises at least one of the promoter regions, or an
     effective part.  The fragment can be obtained from a genomic library of
     wheat and can be fused to suitable genes and markers and inserted into
     suitable vectors for expression in transgenic monocot plants.
     The P2 promoter, found in the second intron, was 2-4 times more active in
     wheat, barley, oat and maize cells that the P1-P2 combination.
AN   1998:256690  HCAPLUS <<LOGINID::20100610>>
DN   128:253799
OREF 128:50155a,50158a
TI   Promoter of wheat wbeI gene for expressing foreign genes in
     monocotyledonous plants
IN   Baga, Monica; Chibbar, Ravindra N.; Kartha, Kutty K.
PA   Baga, Monica, Can.; Chibbar, Ravindra N.; Kartha, Kutty K.
SO   Can. Pat. Appl., 78 pp.
     CODEN: CPXXEB
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.          KIND   DATE        APPLICATION NO.        DATE
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PI   CA 2196834           A1    19971204    CA 1997-2196834        19970205 <--
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US 5866793 A 19990202 US 1996-773251 19961223 <--
PRAI CA 1996-2178016 A 19960603 <--
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)

L12 ANSWER 19 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Characterization of dull1, a maize gene coding for a novel starch synthase
AB The maize dull1 (du1) gene is a determinant of the structure of endosperm starch, and du1-mutations affect the activity of two enzymes involved in starch biosynthesis, starch synthase II (SSII) and starch branching enzyme IIa (SBEIIa). Six novel du1-mutations generated in Mutator-active plants were identified. A portion of the du1 locus was cloned by transposon tagging, and a nearly full-length Du1 cDNA sequence was determined Du1 codes for a predicted 1674-residue protein, comprising one portion that is similar to SSIII of potato, as well as a large unique region. Du1 transcripts are present in the endosperm during the time of starch biosynthesis, but the mRNA was undetectable in leaf or root tissue. The predicted size of the Du1 gene product and its expression pattern are consistent with those of maize SSII. The Du1 gene product contains two repeated regions in its unique N terminus. One of these contains a sequence identical to a conserved segment of SBEs. We conclude that Du1 codes for a starch synthase, most likely SSII, and that secondary effects of du1-mutations, such as reduction of SBEIIa, result from the primary deficiency in this starch synthase.
AN 1998:215485 HCAPLUS <<LOGINID::20100610>>
DN 129:2125
OREF 129:531a,534a
TI Characterization of dull1, a maize gene coding for a novel starch synthase
AU Gao, Ming; Wanat, Jennifer; Stinard, Philip S.; James, Martha G.; Myers, Alan M.
CS Department of Biochemistry and Biophysics, Iowa State University, Ames, IA, 50011, USA
SO Plant Cell (1998), 10(3), 399-412
CODEN: PLCEEW; ISSN: 1040-4651
PB American Society of Plant Physiologists
DT Journal
LA English
OSC.G 100 THERE ARE 100 CAPLUS RECORDS THAT CITE THIS RECORD (100 CITINGS)
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 20 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Comparing the properties of Escherichia coli branching enzyme and maize branching enzyme
AB Escherichia coli glycogen branching enzyme (GBE) and maize starch branching enzymes I (SBEI) and II (SBEII) were expressed in E. coli and purified. E. coli GBE branched amylose at a higher rate than did SBEII, but branched amylose at a lower rate than did SBEI. Similar to SBEI, GBE branched amylopectin at a lower rate than did SBEII. High-performance anion-exchange chromatog. anal. of the branched products produced by BE revealed the min. chain length (cl) required for branching. While GBE and SBEII showed the same min. cl [d.p. (dp) 12] required for branching, SBEI had a slightly higher min. cl (dp 16) requirement for branching. The major differences between GBE and SBE are their specificities in terms of the size of chains transferred. In comparison with SBE, GBE had a much narrower size range of chains transferred and transferred mainly shorter chains. While SBEI and SBEII produced a large number of chains ranging from dp 6 to over dp 30, GBE

predominantly transferred chains ranging from dp 5 to 16 and produced only a very small number of long chains with dp greater than 20. Although it has been reported that SBEI and SBEII preferentially transfer longer and shorter chains, resp. (1), this study further defines the differences between SBEI and SBEII in the size of chains transferred. SBEI predominantly transfers longer chains with dp greater than 10, while producing few shorter chains with dp 3 to 5. In contrast, SBEII preferentially transfers smaller chains with dp 3 to 9, with the most abundant chains being dp 6 and 7. The significance of min. chain-length requirement by SBE is discussed in setting the invariant size of amylopectin cluster size (9 nm).

AN 1997:347385 HCAPLUS <<LOGINID::20100610>>
DN 127:46831
OREF 127:8835a,8838a
TI Comparing the properties of Escherichia coli branching enzyme and maize branching enzyme
AU Guan, Hanping; Li, Ping; Imparl-Radosevich, Jennifer; Preiss, Jack; Keeling, Peter
CS ExSeed Genetics, Agronomy Dep., Iowa State Univ., Ames, IA, 50011, USA
SO Archives of Biochemistry and Biophysics (1997), 342(1), 92-98
CODEN: ABBIA4; ISSN: 0003-9861
PB Academic
DT Journal
LA English
OSC.G 43 THERE ARE 43 CAPLUS RECORDS THAT CITE THIS RECORD (43 CITINGS)
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 21 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat
AB A full-length cDNA (2970 bp) encoding a starch branching enzyme II (SBEII; EC 2.4.1.18) in wheat (Triticum aestivum L. cv Fielder) kernel was isolated from a cDNA library. The translated region of the cDNA predicted a 823 amino acid primary product with a mol. mass of 91.4 kDa. A 54 amino acid transit peptide was postulated to be cleaved from the pre-protein to give a 769 amino acid (85.4 kDa) mature polypeptide, which showed extensive sequence similarity to SBEII sequences characterized from maize, rice and pea. Expression of the isolated cDNA in a BE-deficient E. coli strain demonstrated that it encoded a functional BE. RNA anal. of Sbe2 gene expression during seed development revealed that Sbe2 mRNA levels were highest in young kernels (5-10 days post-anthesis) and declined as the kernels matured.
AN 1997:123840 HCAPLUS <<LOGINID::20100610>>
DN 126:248817
OREF 126:48055a,48058a
TI Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat
AU Nair, Ramesh B.; Baga, Monica; Scoles, Graham J.; Kartha, Kutty K.; Chibbar, Ravindra N.
CS Department of Crop Science and Plant Ecology, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Can.
SO Plant Science (Shannon, Ireland) (1997), 122(2), 153-163
CODEN: PLSCE4; ISSN: 0168-9452
PB Elsevier
DT Journal
LA English
OSC.G 30 THERE ARE 30 CAPLUS RECORDS THAT CITE THIS RECORD (30 CITINGS)

L12 ANSWER 22 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Differential expression and properties of starch-
branching enzyme isoforms in developing wheat endosperm
AB Three forms of starch-branching enzyme (BE)
from developing hexaploid wheat (Triticum aestivum) endosperm have been
partially purified and characterized. Immunol. cross-reactivities
indicate that two forms (WBE-IAD, 88 kDa, and WBE-IB, 87 kDa) are related
to the maize BE I class and that WBE-II (88 kDa) is related to
maize BE II. Comparison of the N-terminal sequences from WBE-IAD
and WBE-II with maize and rice BEs confirms these relationships.
Evidence is presented from the anal. of nullisomic-tetrasomic wheat lines
demonstrating that WBE-IB is located on chromosome 7B and that the WBE-IAD
fraction contains polypeptides that are encoded on chromosomes 7A and 7D.
The wheat endosperm BE classes are differentially expressed
during endosperm development. WBE-II is expressed at a constant
level throughout mid and late endosperm development. In contrast, WBE-IAD
and WBE-IB are preferentially expressed in late endosperm
development. Differences are also observed in the kinetic characteristics of
the enzymes. The WBE-I isoforms have a 2- to 5-fold higher affinity for
amylose than does WBE-II, and the WBE-I isoforms are activated up to
5-fold by phosphorylated intermediates and inorg. phosphate, whereas
WBE-II is activated only 50%. The potential implications of this
activation of BE I for starch biosynthesis are discussed.
AN 1997:73618 HCAPLUS <<LOGINID::20100610>>
DN 126:169149
OREF 126:32649a,32652a
TI Differential expression and properties of starch-
branching enzyme isoforms in developing wheat endosperm
AU Morell, Matthew K.; Blennow, Andreas; Kosar-Hashemi, Behjat; Samuel,
Michael S.
CS Cooperative Res. Cent. Plant Sci., Canberra, ACT 2601, Australia
SO Plant Physiology (1997), 113(1), 201-208
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
OSC.G 90 THERE ARE 90 CAPLUS RECORDS THAT CITE THIS RECORD (90 CITINGS)

L12 ANSWER 23 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Evolutionary conservation and expression patterns of
maize starch branching enzyme I and
IIb genes suggest isoform specialization
AB Expression of the maize (Zea mays L.) starch
branching enzyme (SBE) genes Sbe1 and Sbe2 were
characterized during kernel development and in vegetative tissues. The
onset of Sbe1 and Sbe2 expression during endosperm development
was similar to that of other genes involved in starch biosynthesis (Wx,
Sh2 and Bt2). However, the expression of Sbe2 peaked earlier
than that of Sbe1 in developing endosperm and embryos resulting in a shift
in the ratio of Sbe1 to Sbe2 relative message levels during kernel and
embryo development. Transcripts hybridizing to the Sbe2 probe were not
detectable in leaves kernel and embryo development. Transcripts
hybridizing to the Sbe2 probe were not detectable in leaves or roots which
nonetheless have SBEII enzymic activity, suggesting that there may be
another divergent SBEII-like gene(s) in maize. A similar
expression pattern is shared between the maize genes and
related genes in pea, which together with their evolutionary conservation,
suggests that the SBE isoforms may play unique roles in starch
biosynthesis during plant development.
AN 1996:466120 HCAPLUS <<LOGINID::20100610>>
DN 125:137991
OREF 125:25725a

TI Evolutionary conservation and expression patterns of maize starch branching enzyme I and IIb genes suggest isoform specialization
AU Gao, Ming; Fisher, Dane K.; Kim, Kyung-Nam; Shannon, Jack C.; Guiltinan, Mark J.
CS Dep. of Horticulture, Pennsylvania State Univ., University Park, PA, 16802, USA
SO Plant Molecular Biology (1996), 30(6), 1223-1232
CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer
DT Journal
LA English
OSC.G 52 THERE ARE 52 CAPLUS RECORDS THAT CITE THIS RECORD (52 CITINGS)

L12 ANSWER 24 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Two closely related cDNAs encoding starch branching enzyme from Arabidopsis thaliana
AB Two starch branching enzyme (SBE) cDNAs were identified in an Arabidopsis seedling hypocotyl library using maize Sbe1 and Sbe2 cDNAs as probes. The two cDNAs have diverged 5', and 3' ends, but encode proteins which share 90% identity over an extensive region with 70% identity to maize SBE IIb. Genomic Southern blots suggest that the two cDNAs are the products of single, independent genes, and that addnl., more distantly related SBE genes may exist in the Arabidopsis genome. The two cDNAs hybridize to transcripts which show similar expression patterns in Arabidopsis vegetative and reproductive tissues, including seedlings, inflorescence rachis, mature leaves, and flowers. This is the first report of the identification of cDNAs encoding two closely related starch branching enzymes from the same species.
AN 1996:149142 HCAPLUS <<LOGINID::20100610>>
DN 124:224561
OREF 124:41433a,41436a
TI Two closely related cDNAs encoding starch branching enzyme from Arabidopsis thaliana
AU Fisher, Dane K.; Gao, Ming; Kim, Kyung-Nam; Boyer, Charles D.; Guiltinan, Mark J.
CS Dep. Horticulture, Pennsylvania State Univ., Univ. Park, PA, 16802, USA
SO Plant Molecular Biology (1996), 30(1), 97-108
CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer
DT Journal
LA English
OSC.G 27 THERE ARE 27 CAPLUS RECORDS THAT CITE THIS RECORD (27 CITINGS)

L12 ANSWER 25 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Allelic analysis of the maize amylose-extender locus suggests that independent genes encode starch-branching enzymes IIa and IIb
AB Starch branching enzymes (SBE) catalyze the formation of α-1,6-glucan linkages in the biosynthesis of starch. Three distinct SBE isoforms have been identified in maize (Zea mays L.) endosperm, SBEI, IIa, and IIb. Independent genes have been identified that encode maize SBEI and IIb; however, it has remained controversial as to whether SBEIIa and IIb result from post-transcriptional processes acting on the product of a single gene or whether they are encoded by sep. genes. Thus, 16-isogenic lines carrying independent alleles of the maize amylose-extender (ae) locus, the structural gene for SBEIIb, were analyzed. At 22 days after pollination ae-B1 endosperm expressed little She2b (ae)-hybridizing transcript, and as expected, ae-B1 endosperm also lacked detectable SBEIIb enzymic activity,. Also, ae-B1 endosperm contained

SBEIIa enzymic activity, strongly supporting the hypothesis that endosperm SBEIIa and IIb are encoded by sep. genes. Furthermore, addition to encoding the predominant Sbe2b-hybridizing message expressed in endosperm, the ae gene also encodes the major She2b-like transcript expressed in developing embryos and tassels.

AN 1996:119513 HCAPLUS <<LOGINID::20100610>>
DN 124:170828
OREF 124:31587a,31590a
TI Allelic analysis of the maize amylose-extender locus suggests that independent genes encode starch-branching enzymes IIa and IIb
AU Fisher, Dane K.; Gao, Ming; Kim, Kyung-Nam; Boyer, Charles D.; Guiltinan, Mark J.
CS Biotechnol. Inst., Pennsylvania State Univ., University Park, PA, 16802, USA
SO Plant Physiology (1996), 110(2), 611-19
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
OSC.G 39 THERE ARE 39 CAPLUS RECORDS THAT CITE THIS RECORD (39 CITINGS)

L12 ANSWER 26 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Starch branching enzymes belonging to distinct enzyme families are differentially expressed during pea embryo development
AB CDNA clones for two isoforms of starch branching enzyme (SBEI and SBEII) have been isolated from pea embryos and sequenced. The deduced amino acid sequences of pea SBEI and SBEII are closely related to starch branching enzymes of maize, rice, potato and cassava and a number of glycogen branching enzymes from yeast, mammals and several prokaryotic species. In comparison with SBEI, the deduced amino acid sequence of SBEII lacks a flexible domain at the N-terminus of the mature protein. This domain is also present in maize SBEII and rice SBEIII and resembles one previously reported for pea granule-bound starch synthase II (GBSSII). However, in each case it is missing from the other isoform of SBE from the same species. On the basis of this structural feature (which exists in some isoforms from both monocots and dicots) and other differences in sequence, SBEs from plants may be divided into two distinct enzyme families. There is strong evidence from our own and other work that the amylopectin products of the enzymes from these two families are qual. different. Pea SBEI and SBEII are differentially expressed during embryo development. SBEI is relatively highly expressed in young embryos while maximum expression of SBEII occurs in older embryos. The differential expression of isoforms which have distinct catalytic properties means that the contribution of each SBE isoform to starch biosynthesis changes during embryo development. Qual. measurement of amylopectin from developing and maturing embryos confirms that the nature of amylopectin changes during pea embryo development and that this correlates with the differential expression of SBE isoforms.
AN 1995:459734 HCAPLUS <<LOGINID::20100610>>
DN 123:136225
OREF 123:24081a,24084a
TI Starch branching enzymes belonging to distinct enzyme families are differentially expressed during pea embryo development
AU Burton, Rachel A.; Bewley, J. Derek; Smith, Alison M.; Bhattacharyya, Madan K.; Tatge, Helma; Ring, Steve; Bull, Vicky; Hamilton, William D. O.; Martin, Cathie
CS John Innes Centre, John Innes Institute, Norwich, NR4 7UH, UK
SO Plant Journal (1995), 7(1), 3-15
CODEN: PLJUED; ISSN: 0960-7412
DT Journal

LA English
OSC.G 91 THERE ARE 91 CAPLUS RECORDS THAT CITE THIS RECORD (91 CITINGS)

L12 ANSWER 27 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Expression of branching enzyme II of maize endosperm in Escherichia coli
AB A cDNA clone encoding maize branching enzyme II (BEII) has been independently isolated from a maize endosperm cDNA library. The deduced protein sequence of maize BEII was compared with that of BE from diverse sources. The gene encoding mature BEII of maize endosperm has been expressed in E. coli using the T7 promoter. The expressed BEII was purified to near homogeneity so that amylolytic activity and bacterial BE could be completely eliminated from the BE preparation The expressed enzyme showed very similar properties to those of bEII purified from developing maize endosperm. This result confirmed our earlier report that BEII had a lower rate of branching amylose and the rate of branching amylopectin was twice that of branching amylose. This study also showed a greater advantage of purifying BEII from the bacterial expression system than from developing maize endosperm. Most importantly, this study has established a useful tool to study the structure-function relationships of the maize BE using site-directed mutagenesis.
AN 1995:140589 HCAPLUS <<LOGINID::20100610>>
DN 123:4386
OREF 123:915a,918a
TI Expression of branching enzyme II of maize endosperm in Escherichia coli
AU Guan, Han Ping; Baba, Tadashi; Preiss, Jack
CS Department Biochemistry, Michigan State University, East Lansing, MI, 48824, USA
SO Cellular and Molecular Biology (Paris) (1994), 40(7), 981-8
CODEN: CMOBEF; ISSN: 0145-5680
PB C.M.B. Association
DT Journal
LA English
OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)

L12 ANSWER 28 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Genetic isolation, cloning, and analysis of a Mutator-induced, dominant antimorph of the maize amylose extender1 locus
AB The authors report the genetic identification, mol. cloning, and characterization of a dominant mutant at the amylose extender1 locus, Ae1-5180. The identities of the authors' clones are corroborated by their ability to reveal DNA polymorphisms between seven wild-type revertants from Ae1-5180 relative to the Ae1-5180 mutant allele and between four of five independently derived, Mutator (Mu)-induced recessive ae1 alleles relative to their resp. wild-type progenitor alleles. The Ae1-5180 mutation is associated with two Mu1 insertions flanked by complex rearrangements of ae1-related sequences. One of the Mu1 elements is flanked by inverted repeats of ae1-related DNA of at least 5.0 kb in length. This Mu1 element and at least some of this flanking inverted repeat DNA are absent or hypermethylated in six of seven wild-type revertants of Ae1-5180 that were analyzed. The second Mu1 element is flanked on one side by the 5.0-kb ae1-specific repeat and on the other side by a sequence that does not hybridize to the ae1-related repeat sequence. This second Mu1 element is present in revertants to the wild type and does not, therefore, appear to affect ae1 gene function. A 2.7-kb ae1 transcript can be detected in wild-type and homozygous ae1-Ref endosperms 20 days after pollination. This transcript is absent in endosperms containing one, two, or three doses of Ae1-5180. This result is consistent with a suppression model to explain the dominant gene action of

Ae1-5180 and establishes Ae1-5180 as an antimorphic allele. Homozygous wild-type seedlings produce no detectable transcript, indicating some degree of tissue specificity for ael expression. Sequence analyses establish that ael encodes starch branching enzyme II.

AN 1994:550052 HCAPLUS <<LOGINID::20100610>>
DN 121:150052
OREF 121:26949a,26952a
TI Genetic isolation, cloning, and analysis of a Mutator-induced, dominant antimorph of the maize amylose extender1 locus
AU Stinard, Philip S.; Robertson, Donald S.; Schnable, Patrick S.
CS Dep. Agron., Iowa State Univ., Ames, IA, 50011, USA
SO Plant Cell (1993), 5(11), 1555-66
CODEN: PLCEEW; ISSN: 1040-4651
DT Journal
LA English
OSC.G 62 THERE ARE 62 CAPLUS RECORDS THAT CITE THIS RECORD (62 CITINGS)

L12 ANSWER 29 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Modulating the quantity and quality of starch synthesis in plants by placing the gene for a starch-metabolizing enzyme under control of a regulated promoter
AB A method of producing a plant with switchable starch-synthesizing ability by stably incorporating a target gene for an enzyme involved in a starch or glycogen biosynthetic pathway and under the control of a regulated promoter into the genome of a recipient plant. A plant with controllable starch-synthesizing ability may have switchable starch yield, and/or switchable starch quality. Starch or glycogen biosynthetic enzymes include soluble starch synthase, branching enzyme , glycogen synthase, ADP-glucose pyrophosphorylase, self-glucosylating protein, glycogenin and amylogenin. DNA constructs for use in this method are described, as well as plants transformed with said DNA constructs, the seeds and progeny of such plants, and hybrids whose pedigree includes such plants. The examples demonstrate the functioning of the chemical-inducible promoter of the gene for the 27 kd subunit of glutathione-S-transferase II in maize endosperm and discuss the construction of appropriate expression vectors.
AN 1994:530242 HCAPLUS <<LOGINID::20100610>>
DN 121:130242
OREF 121:23445a,23448a
TI Modulating the quantity and quality of starch synthesis in plants by placing the gene for a starch-metabolizing enzyme under control of a regulated promoter
IN Keeling, Peter Lewis
PA Zeneca Ltd., UK
SO PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9411520	A2	19940526	WO 1993-GB2305	19931109 <--
	WO 9411520	A3	19940804		
	W: AU, BB, BG, BR, BY, CA, CZ, FI, HU, JP, KP, KR, KZ, LK, LV, MG, MN, MW, NO, NZ, PL, RO, RU, SD, SK, UA, US, VN				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9454285	A	19940608	AU 1994-54285	19931109 <--
PRAI	GB 1992-23454	A	19921109	<--	
	WO 1993-GB2305	W	19931109	<--	

OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (22 CITINGS)
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 30 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Expression of branching enzyme I of maize endosperm in Escherichia coli
AB The gene encoding for mature branching enzyme (BE) I (BEI) of maize (Zea mays L.) endosperm has been expressed in Escherichia coli using the T7 promoter. The expressed BEI was purified to near homogeneity so that amylolytic activity and bacterial BE could be completely eliminated from the BE preparation The recombinant enzyme showed properties very similar to those of BEI purified from developing maize endosperm with respect to branching amylose and amylopectin. This result confirmed the authors' earlier report that maize endosperm BEI had a higher rate of branching amylose and a much lower rate (less than 10% of that of branching amylose) of branching amylopectin. This study also showed a great advantage in purifying BE from the bacterial expression system rather than from developing maize endosperm. Most important, this study has established the system with which to study the structure-function relationships of the maize BEI using site-directed mutagenesis.
AN 1994:502618 HCAPLUS <<LOGINID::20100610>>
DN 121:102618
OREF 121:18339a,18342a
TI Expression of branching enzyme I of maize endosperm in Escherichia coli
AU Guan, Han Ping; Baba, Tadashi; Preiss, Jack
CS Dep. Biochem., Michigan State Univ., East Lansing, MI, 48824, USA
SO Plant Physiology (1994), 104(4), 1449-53
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
OSC.G 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)

L12 ANSWER 31 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Comparison of soluble starch synthases and branching enzymes from leaves and kernels of normal and amylose-extender maize
AB Soluble starch synthases (SS) and branching enzymes (BE) from 20-day-old maize leaves and 22-day-old seeds of normal and amylose-extender (ae) were purified by DEAE-cellulose chromatog. Elution profiles of leaf exts. showed 1 major SS and 2 BE fractions from both genotypes. The SS fractions from normal and ae leaf exts. were capable of citrate-stimulated starch synthesis and had different reaction rates with various primers. The 2 BE fractions from normal leaf exts. differed significantly from each other but not when compared to the same BE from ae. Comparison of BE fractions from ae and normal leaves showed no differences based on chromatog., kinetic, and immunol. properties. Comparison of the leaf enzymes with endosperm enzymes showed major differences. Leaf exts. did not contain SSII or BEIIb observed in endosperm exts. Developing ae endosperm lacked BEIIb activity and ae was the structural gene for BEIIb. The tissue-specific expression of BEIIb in the endosperm provided the basis for explaining the tissue-specific expression of ae. It was proposed that as BEIIb is expressed in the endosperm, but not leaves, allelic substitution at the ae locus modifies only endosperm starch synthesis.
AN 1990:94355 HCAPLUS <<LOGINID::20100610>>
DN 112:94355
OREF 112:15955a,15958a
TI Comparison of soluble starch synthases and branching enzymes from leaves and kernels of normal and amylose-extender maize

AU Dang, Peter L.; Boyer, Charles D.
CS Dep. Hort., Pennsylvania State Univ., University Park, PA, 16802, USA
SO Biochemical Genetics (1989), 27(9-10), 521-32
CODEN: BIGEBA; ISSN: 0006-2928
DT Journal
LA English
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L12 ANSWER 32 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Maize leaf and kernel starch synthases and starch branching enzymes
AB Soluble starch synthases and branching enzymes were partially purified from developing leaves and kernels of maize using DEAE-cellulose chromatog. One form of starch synthase and 2 forms of branching enzyme were detected in leaves as compared to 2 forms of starch synthase and 3 forms of branching enzyme isolated from the kernels. The starch synthase fraction from the leaves and the 1st starch synthase fraction from the kernels showed greater activity in reactions containing various glycogens as primers than in those containing amylopectin. In addition, both were capable of synthesizing a polyglucan in the absence of an added primer but in the presence of Na citrate and bovine serum albumin (citrate-stimulated starch synthesis). The 2nd starch synthase fraction from kernels showed greater activity with amylopectin as primer and had no citrate-stimulated activity. The leaf enzyme and endosperm starch synthase I are suggested to be the same enzyme and constitutively expressed. Branching enzymes from leaves and kernels differed not only in their elution profiles but also their stimulation of phosphorylase a (assay A) and amylose branching (assay B) activities. A minor branching enzyme fraction from leaves (leaf branching enzyme I) eluted from the DEAE-cellulose column after the addition of a salt gradient, whereas branching enzyme I from kernels eluted in the buffer wash prior to the application of the gradient. However, the ratios of assay A to assay B suggested that branching enzyme I from leaves was catalytically similar to branching enzyme I from the kernels. The major leaf branching enzyme (branching enzyme II) eluted at the same position from the DEAE-cellulose column as endosperm branching enzyme IIa. These enzymes had similar ratios of activity (assay A/assay B). The cross-reaction of leaf branching enzymes with antisera prepared against maize endosperm branching enzymes in immunodiffusion expts. and enzyme activity neutralization expts. further demonstrated the relationship of the leaf and endosperm branching enzymes.
AN 1988:434288 HCAPLUS <<LOGINID::20100610>>
DN 109:34288
OREF 109:5733a,5736a
TI Maize leaf and kernel starch synthases and starch branching enzymes
AU Dang, Peter L.; Boyer, Charles D.
CS Dep. Hortic., Pennsylvania State Univ., University Park, PA, 16802, USA
SO Phytochemistry (1988), 27(5), 1255-9
CODEN: PYTCAS; ISSN: 0031-9422
DT Journal
LA English
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)

L12 ANSWER 33 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN
TI Evidence for independent genetic control of the multiple forms of maize endosperm branching enzymes and starch synthases
AB Soluble starch synthase and starch-branching enzymes in exts. from kernels of 4 corn genotypes were compared. Exts. from normal (nonmutant) corn were found to contain 2 starch synthases and 3 branching

enzyme fractions. The different fractions could be distinguished by chromatog. properties and kinetic properties under various assay conditions. Kernels homozygous for the recessive amylose-extender (ae) allele were missing branching enzyme IIb. In addition, the citrate-stimulated activity of starch synthase I was reduced. This activity could be regenerated by the addition of branching enzyme to this fraction. No other starch synthase fractions were different from normal enzymes. Exts. from kernels homozygous for the recessive dull (du) allele were found to contain lower branching enzyme IIa and starch synthase II activities. Other fractions were not different from the normal enzymes. Anal. of exts. from kernels of the double mutant ae du indicated that the 2 mutants act independently. Branching enzyme IIb was absent and the citrate-stimulated reaction of starch synthase I was reduced but could be regenerated by the addition of branching enzyme (ae properties) and both branching enzyme IIa and starch synthase II were greatly reduced (du properties). Starch from ae and du endosperms contains higher amylose (66 and 42%, resp.) than normal endosperm (26%). In addition, the amylopectin fraction of ae starch is less highly branched than amylopectin from normal or du starch. The above observations suggest that the alterations of the starch may be accounted for by changes in the soluble synthase and branching enzyme fractions.

AN 1981:458224 HCAPLUS <<LOGINID::20100610>>
DN 95:58224
OREF 95:9805a,9808a
TI Evidence for independent genetic control of the multiple forms of maize endosperm branching enzymes and starch synthases
AU Boyer, Charles D.; Preiss, Jack
CS Dep. Biochem. Biophys., Univ. California, Davis, CA, 95616, USA
SO Plant Physiology (1981), 67(6), 1141-5
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
OSC.G 56 THERE ARE 56 CAPLUS RECORDS THAT CITE THIS RECORD (56 CITINGS)